



"Replacement Sheet"

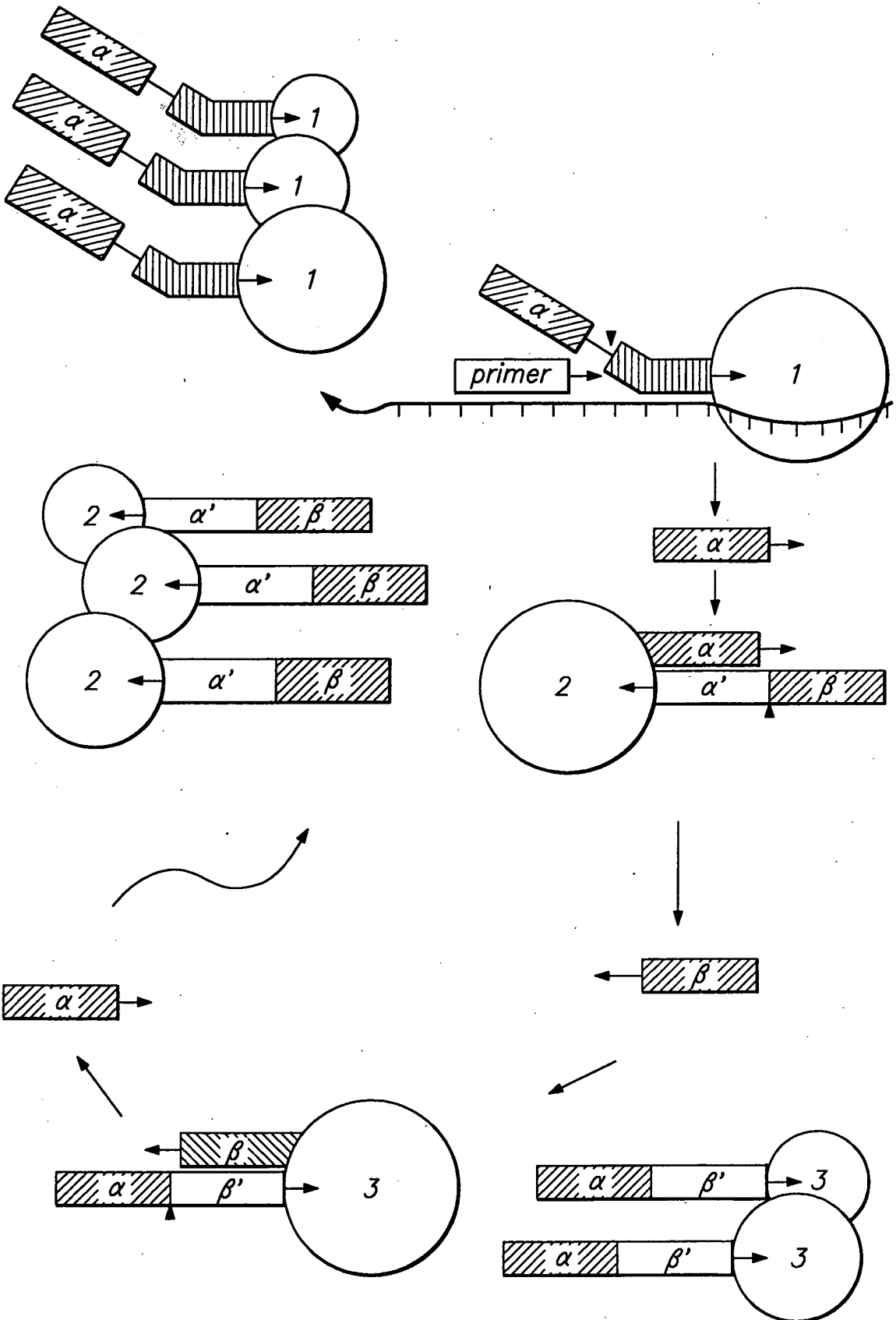
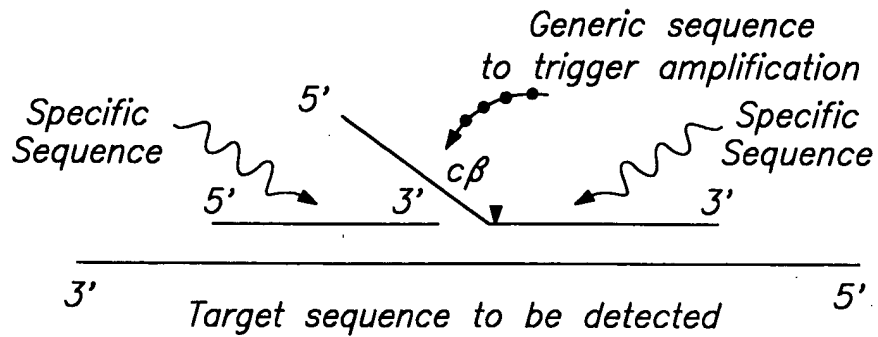
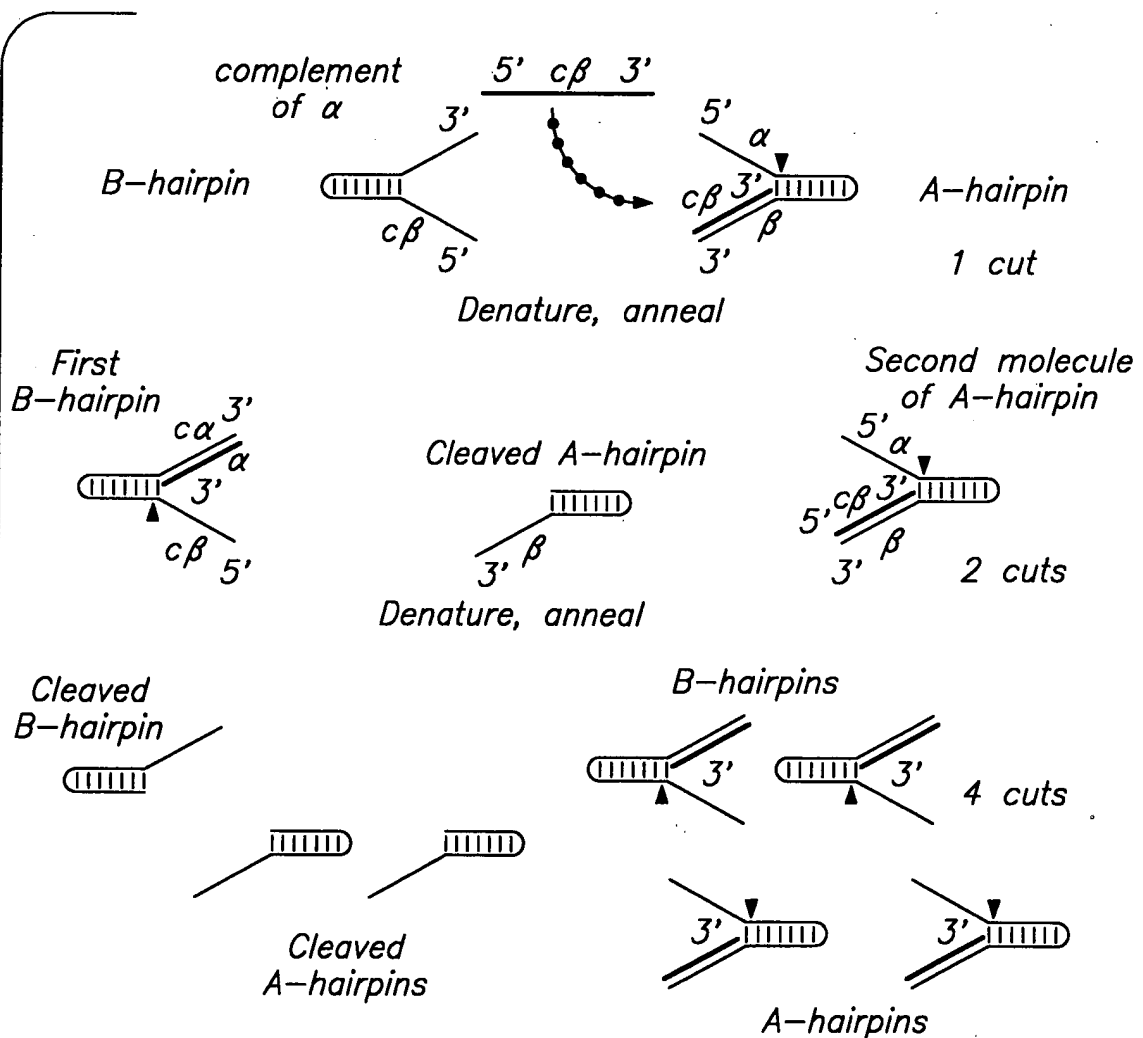


FIG. 1A

FIG. 1B



PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION

FIG. 2A

MAJORITY	[SEQ ID NO:7]	ATGXXGGCGATGCTTCCCTCTTGAGCCGAAGGCCGGCTCCTCCTGCTGGACGGCCACCACTGGCGT	
DNAPTAD	[SEQ ID NO:1]	..AG..G.....G.....G.....	70
DNAPTFL	[SEQ ID NO:2]G.....C..G.....	67
DNAPTTH	[SEQ ID NO:3]	..GA.....G.....A.....	70
MAJORITY		ACCGCAGCTTCTTGGCGCTGAAGGGCTCAGCACCAGCGGGCGGAACCGTGCAGGGCTCTACGGCTT	
DNAPTAD	GA.....G.....G.....G.....	140
DNAPTFL	T.....C.....C.....C..T.....	137
DNAPTTH	G.....G.....	140
MAJORITY		CGCGAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGACXXGGGGTGTGTGTCTTGAGCCCAAG	
DNAPTAD	G.....G.....A.....A.....	207
DNAPTFL	A.....GT..T.....	204
DNAPTTH	T..AA..C..GT.....	210
MAJORITY		GGCCCTCCTCGCGCAGAGGCTACGAGGCTACAAGGGGGCGGGCCCAAGCCCGAGGACTTC	
DNAPTAD	G..GG.....G.....	277
DNAPTFL	G.....G.....	274
DNAPTTH	GA.....G.....C.....C.....	280
MAJORITY		CGCGGAGCTGGCGCTCATCAAGGAGCTGCTGAGCCTCCTGGGGCTTGGGGCTCGAGGTCGCCGGCTA	
DNAPTAD	A.....G.....G.....G.....	347
DNAPTFL	G.....T.....A..C.....T..G..G.....T.....	344
DNAPTTH	T.....T..A..G.....	350

MAJORITY	[SEQ ID NO: 73]	CGAGGGGAGCGAGCTXGTGGCCACCCCTGGCCAGAAGCGCGGAAAAAGAGGGCTACGAGCTGGCATCCTC	
DNAPTAD	[SEQ ID NO: 13]C.....G.....C.....C.....C.....	417
DNAPTFL	[SEQ ID NO: 23]	T.....G.....CG.....	414
DNAPTTH	[SEQ ID NO: 33]T.....G.....	420
MAJORITY		ACGGCCGAGCGGACCTCTACGAGCTCCTTCCGAGCGCATCGGGCTCCTCGACCCCGAGGGGTACCTCA	
DNAPTAD	AAA.....T.....CA.....	487
DNAPTFL		T.....G.....G.....G.....T.....G.....	484
DNAPTTH	A.....G.....G.....CG.....	490
MAJORITY		TGACCCCGGGCGTGGCTTGGGAGAGTACGGCCCTGAGCCCGGAGCACTGGTGGACTACCGGGCCCTGGC	
DNAPTAD	C.....A.....C.....C.....CG.....A.....	557
DNAPTFL	AC.....C.....C.....	554
DNAPTTH	A.....G.....T.....C.....C.....T.....	560
MAJORITY		GGGGAGCCGCTCGGACAACCTCCGGGGGTGAAGGGCATCGGGGAGAAGACGGCCGXGAAGCTCCTCXAG	
DNAPTAD		C.....GAG.....T.....G.....GAG.....T.....GG.....	627
DNAPTFL	G.....T.....A.....G.....A.....G.....A.....CGC.....	624
DNAPTTH	TC.....A.....	630
MAJORITY		GAGTGGGGGAGCGCTGGAAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC...CXTCGGGGAGAGA	
DNAPTAD	GC.....C.....A.....	694
DNAPTFL	T.....C.....A.....T.....T.....G.....C.....	691
DNAPTTH		A.....A.....A.....A.....A.....G.....	700

FIG. 2C

MAJORITY	[SEQ ID NO:7]	TCGAGGCCACATGGAXGACCTGAXGCTCTGCTGGAGCTXTGCCAGGTGGCGACCGACCTGGCCCTGGA	
DNAPTAO	[SEQ ID NO:1]	...T.....C..T...A.....C..GG..A.....	764
DNAPFL	[SEQ ID NO:2]	...GGG...G.C...GCC..T...C..A...T.....A...T.....	761
DNAPTH	[SEQ ID NO:3]	...A.....C...A.....C..G.....T.....C...G.....	770
MAJORITY		GGTGGACTTCGCCAAGXGGCGGAGCCCGACCGGAGGGGCTTAGGGCTTCTGGAGAGCTGGACTT	
DNAPTAO		...A.....A.....A.....A.....T.....	834
DNAPFL		...GG.G.C.C..GACA..A..T.....T..GC...T...C..T.....	831
DNAPTH		...C...C..G.....C.....C.....	840
MAJORITY		GGCAGCCTCCTCCACGAGCTCGGCTCTCTGGAGGCCCCCAAGGCCCTGGAGAGGCCCCCTGGCCCCGG	
DNAPTAO		...T.....AA.....G.....G.....GCCA.....T.....	904
DNAPFL		...A.....G.....G.....GCCA.....T.....	901
DNAPTH		...G.....GCCG.....	910
MAJORITY		CGGAGGGGCTTGGTGGCTTGTCTTCCGCGCCGAGGCCATGTGGCCGAGCTCTGGCCCTGGC	
DNAPTAO		...G.....AG.....T.....	974
DNAPFL		...T..T.....TC.T.....T.....	971
DNAPTH		...G.....C.....G.....AAA.....	980
MAJORITY		CGCCGCCAGGAGGGCCGGCTGCACCGGCGACGACCCCTTAXGGGCTXAGGGACCTXAAGGAGGTG	
DNAPTAO		...G.....C..C..G..T..A..AA..C...C.....G.....C.....	1044
DNAPFL		...T.GG..GT.....G..CC...T.....A.....G.....G.....T.....G.....	1041
DNAPTH		...TG.....C.....G.....G.....GGC...G..A..A.....C.....C.....	1050

FIG. 2D

MAJORITY [SEQ ID NO:7] GGGGGXCTGCTGCCCAAGGACCTGGCGGTTTGGCCCTGAGGAGGGCCCTXGACCTCTGCGCGGGGAGC

DNAPTAD [SEQ ID NO:12]G..T.....A.....AG.....C.....A.....T..G.....CC.....C..... 1114
DNAPTFL [SEQ ID NO:23]AA.....G.....G.....C.....C.....G.....T..C.....A..A..... 1111
DNAPTTH [SEQ ID NO:33]C.....C.....C.....C.....TC.....G..A.....G..... 1120

MAJORITY ACCCATGCTCTCGCTACCTCTGAGCCCTCCAACACGACCCCGAGGGGCTGGCCCGGCGCTACGG

DNAPTADT.....T.....T.....T.....T.....T.....T.....T..... 1184
DNAPTFLG.....T.....T.....T.....T.....T.....T.....T..... 1181
DNAPTTHG.....G.....G.....G.....G.....G.....G.....G..... 1190

MAJORITY GGGGAGTGGACGGAGGAXGCGGGGAGCGGGCCCTCCTXTCGAGAGGCTCTCCXGAGCCTXXXGGAG

DNAPTADG.....G.....G.....G.....G.....G.....G.....G..... 1254
DNAPTFLT.....T.....T.....T.....T.....T.....T.....T..... 1251
DNAPTTHC..C..G..G..C..G..C..G..C..G..CAT..G.....CCTTA.. 1260

MAJORITY GCGCTGAGGGGAGGAGGCTCCTTGCTTACCAAGAGCTGGAGAGCCCTTTCCGGGCTCCTGG

DNAPTADA.....G.....G.....G.....G.....G.....G.....GCT..... 1324
DNAPTFLA.....A..A..AC..C..G.....G.....G.....GT..... 1321
DNAPTTHC.....A.....C.....C.....A.....A.....C.....C..... 1330

MAJORITY CCCACATGGAGGGCAGCGGGGTXCGGCTGGAGCTGGCTACCTCCAGGCGCCTXTCCTGGAGGTGGCGGA

DNAPTADG.....G.....G.....G.....G.....G.....G.....G..... 1394
DNAPTFLGG.....C.....C.....C.....C.....C.....C.....A..C..... 1391
DNAPTTHC.....A.....A.....T.....T.....T.....T.....C..T..... 1400

FIG. 2E

MAJORITY [SEQ ID NO:7]		GGAGATCGCGCGCCTCGAGGAGAGCTCTCGGCCTGCGCGCGACCCCTCAACCTCAACTCCGGGAC	
DNAPTAA	[SEQ ID NO:12]GC.....CG.....	1464
DNAPTFL	[SEQ ID NO:23]	...G.G...AG..G.....	1461
DNAPTTH	[SEQ ID NO:33]	1470
MAJORITY		CAGCTGGAAAGGCTGCTCTTGACGAGCTXGGGCTTCGGCGCATCGGCAAGACGGAGAAGACXGCCAAGC	
DNAPTAA	G.....A.....	1534
DNAPTFL	GC.....G..C..G..T.....	1531
DNAPTTH	TA.....T..G..G.....C..A.....A.....	1540
MAJORITY		GCTCGACCAAGCGCGCCCTGCTGGAGGCCCTXCGXAGGCCCAACCCGATCGTGAGAAGATCTGCAGTA	
DNAPTAA	G.....G.....C..C.....	1604
DNAPTFL	T.....G..A.....CGCG.....	1601
DNAPTTH	G.....A..G.....C.....C.....C.....	1610
MAJORITY		CGGGAGCTCAGCAAGCTCAAGAACAGACCTACATXGAGCGCGCTGCCXGCTGCTGCACCCGAGGACGGGC	
DNAPTAA	G.....G.....T.....T.....G..A.....A.....	1674
DNAPTFL	A.....A.....C..G..G.....A.....C.....	1671
DNAPTTH	G.G.....C..AAG.....G.....	1680
MAJORITY		CGGCTCGACACCGCGCTCAACGAGACGGCCACGGCCAGCGCTTAGTAGCTCGGACCCGACCTGC	
DNAPTAA	A.....A.....T.....C.....	1744
DNAPTFL		...G.....C.....TCG.....	1741
DNAPTTH	G.....	1750

FIG. 2F

MAJORITY	[SEQ ID NO: 7]	AGAACATCGCCGCTCCGACGCCXCTGGGCGAGAGGATCCCGCGGCCCTTGTGGCGGAGGAGGXTGGGT	
DNAPTAD	[SEQ ID NO: 1]G..T..G.....A..C.....G...C.	1814
DNAPTFL	[SEQ ID NO: 2]G.....T.....C..C.....A.....C.....	1811
DNAPTTR	[SEQ ID NO: 3]CT.....C.....T.....G	1820
MAJORITY		GTGCTGGCCCTGGACTATAGCCAGATAGAGCTCGGGCTCTGGCCCACTCTCGGGGACGGAACCTG	
DNAPTAD		A.....A.....G.....C.....	1884
DNAPTFL		.C.....T..T.....C.....T.....T.....	1881
DNAPTTR	C.....C.....A.....	1890
MAJORITY		ATCGGGCTCTCAAGAGGGGAGGACATGCACACCGAGACCGCAGCTGGATGTCGGCGTCCGCCCGG	
DNAPTAD	G.....GG.....G.....	1954
DNAPTFL	T.....A.....T.....C.	1951
DNAPTTR		..A.....A.....A.....	1950
MAJORITY		AGGGCGTGGACCCCTGATGGCGCGGGCGGCAAGACCATCACTTGGGGTCTCTACGGCATGTCCGC	
DNAPTAD	A.....G.....G.....	2024
DNAPTFL		.A..G..A.....T.....G.....G.....	2021
DNAPTTR	G..G..G.....C.....	2030
MAJORITY		GCACGGCTCTCCAGGAGCTTGCATCCGCTACGAGGAGGGGTGGCCTTCATTGAGCGCTACTTCAG	
DNAPTAD	A.....T.....T.....CCA.....T.....	2094
DNAPTFL	GG.....T.....	2091
DNAPTTR		...TA..G.....T..A.....A	2100

FIG. 2G

MAJORITY [SEQ ID NO:7] AGCTTCGGCAAGCTGGGGCGCTGATTGAGAGACCCTGGAGAGGGGAGGAGGGCGGGTACGTGAGA			
DNAPTAA	[SEQ ID NO:13]A.....	2154
DNAPTFL	[SEQ ID NO:23]A.....GG.....G.....C.....G.....G.....T.....	2161
DNAPTTR	[SEQ ID NO:33]A.....A.....A.....G.....A.....C.....A.....	2170
MAJORITY CCCTCTGGGGCGGGCGCTACGTGGCGGACCTCAAGCGCGGGTGAAGAGCGTGGGGAGCGCGCGGA			
DNAPTAA	C.....A.....AG.....G.....	2234
DNAPTFL	T.....	2231
DNAPTTR	AA.....AA.....CA.....C.....	2240
MAJORITY GCGCATGGCCTTCAACATGGCGCTCGAGGGCACCAGCGGACCTCATGAAGCTGGCCATGGTGAAGCTC			
DNAPTAA	G.....T.....	2304
DNAPTFL	G.....CG.....T.....	2301
DNAPTTR	C.....	2310
MAJORITY TTCGGCGCGCTXCAGGAATGGGGCGAGATGCTCTXCAGGTCACGACGAGCTGCTCCTCGAGGCC			
DNAPTAA	A.....GG.....T.....	2374
DNAPTFL	T.....C.....G.....TT.....G.....G.....	2371
DNAPTTR	G.....G.....G.....C.....G.....CG.....G.....	2380
MAJORITY CCAAGAGCGGGCGGAGCGXGCTGGCGCCTTGGCCAAAGAGCTCATGGAGGGGTCTATGCCCTGGCCGT			
DNAPTAA	A.....A.....CG.....CGCG.....G.....	2444
DNAPTFL	G.....C.....AG.....A.....G.....CG.....GAG.....	2441
DNAPTTR	C.....C.....C.....A.....G.....C.....AA.....C.....C.....	2450

FIG. 2H

MAJORITY	[SEQ ID NO:7]	GGCGCTGGAGCTGGAGCTGGGATGGGGAGGACTGGCTCTCGGCGAAGGAGTAG
DNAPTAA	[SEQ ID NO:1]A.....GA
DNPTFL	[SEQ ID NO:2]CG.....
DNPTTH	[SEQ ID NO:3]T.....GT...

FIG. 3A

MAJORITY	[SEQ ID NO:8]	MXAMLPLFEPRGRVLLVDGHLAYRTFFALKGLTTSRGEPUQAVYGFAKSLKALKEDG-DAVXVVFDAK	
TAQ PRO	[SEQ ID NO:4]	.RG.....H.....	69
TFL PRO	[SEQ ID NO:5]	68
TTR PRO	[SEQ ID NO:6]	.E.....YK.F.....	70
MAJORITY		APSFREAYEAYKAGRPTPEDFPROLALIKELVDLGLXRLVPGYEADDVLATLAKKAKEGYEVRIL	
TAQ PRO	GG.....A.....S.....	139
TFL PRO	V.....F.....R.....	138
TTR PRO	FT.....	140
MAJORITY		TADRDLYLLSDRIAVLHPEGYLLTPAWLWEKYGLRPEQWVDYRALXGDPSONLPGVKGIGEKTAKKLLX	
TAQ PRO		..K.....H.....D.A.....T.E.....R..E	209
TFL PRO	E..I.....Y.....A.....I.....QR.IR	208
TTR PRO	V..V.....H...E.....F..V.....L...K	210
MAJORITY		EWGSLLENLKNLDRVKP-XXREKIXAHMEDLXLSXLSXVRTDLPLEVDFAXRREPDRGLRAFLERLEF	
TAQ PRO	A.....L..Al...L...D..K..WD.AK.....K.....R.....	278
TFL PRO	FOH.O...SL..LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTR PRO	ENV...K.L...R..LE..R.....L.OG.....	280
MAJORITY		GSLHEFGLEXPKALEAPWPPEGAFVGFVLSRPERMMAELLALAARRXGRVHRAXDPLXGLROLKEV	
TAQ PRO	S.....K.....D.....G.....PE.YKA.....A	348
TFL PRO	G..A.....L..SF.....G.WE..I..Q...R.....G.	347
TTR PRO	A.AP.....K.....C.D.....A...A..K.....	350

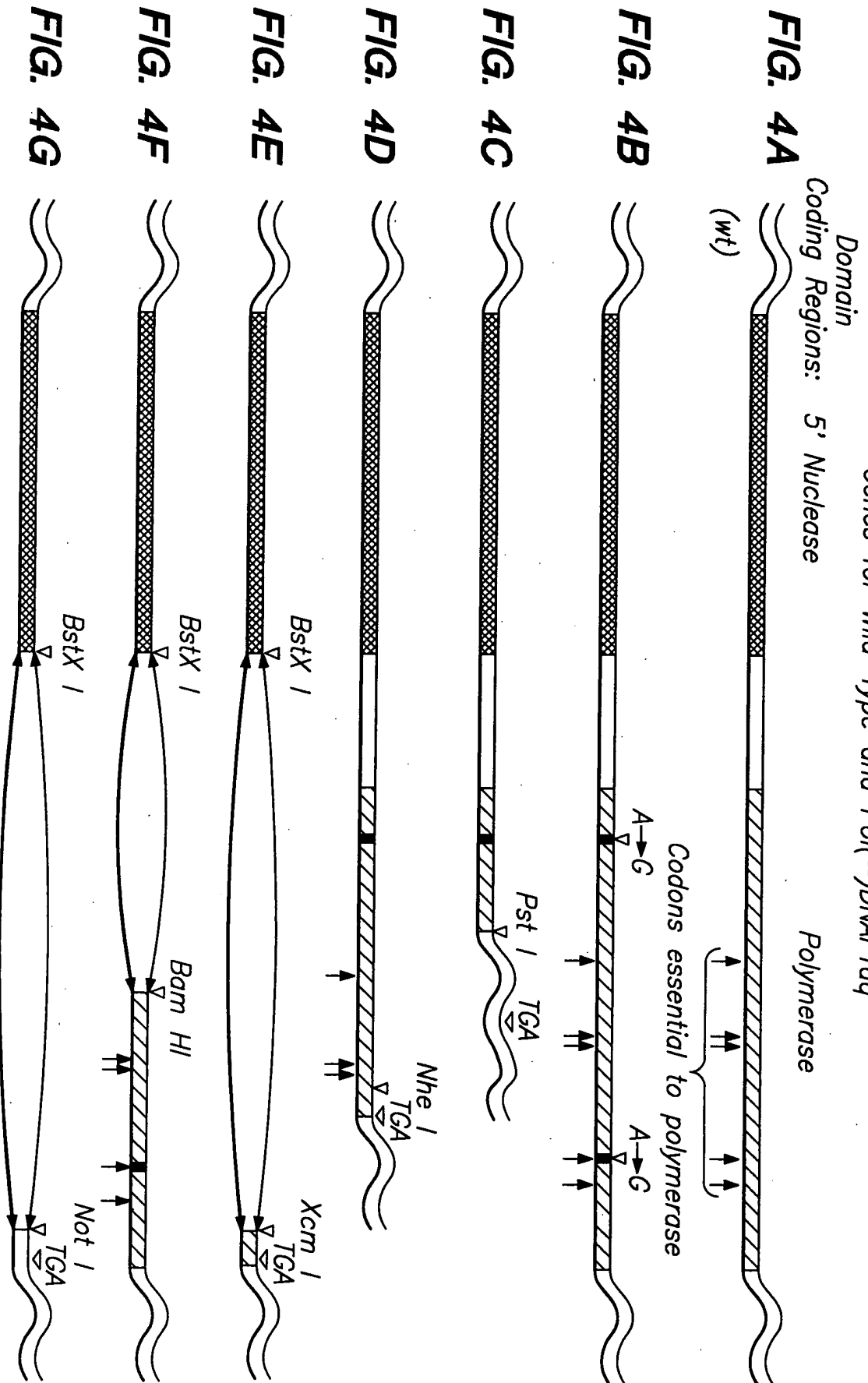
FIG. 3B

MAJORITY	[SEQ ID NO:8]	RGLLAKDLAVLALREGLDXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEADAGERALLSERLFXNLXX	
TAQ PRO	[SEQ ID NO:4]S.....G.P.....E.....A.....A.....A.....WG	418
TFL PRO	[SEQ ID NO:5]I.....F.E.....F.....A.....OT.KE	417
TTH PRO	[SEQ ID NO:6]S.....V.....AH.....HR..LK	420
MAJORITY		RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLEEEVRLAGHPFLNSRD	
TAQ PRO	R..R..A.....R.....A..A.....A.....	488
TFL PRO	K.....E.....R.....EA.V.Q.....	487
TTH PRO	K.....H.....L.....	490
MAJORITY		QLERVLFDLGLPAIGKTEKTGKRSTSAVLEALREAHPIVEKILQYRELTKLKNITYDPLPLVHPRTG	
TAQ PRO	DR.....S.....D.I.....	558
TFL PRO	R..L..Q.....H.....V.....S.....K.....	557
TTH PRO	A..A.....	560
MAJORITY		RLHTRFNQTATATGRSSSDPNLONI PVRTPLGORIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL	
TAQ PRO	L.....L.....	628
TFL PRO	V..V.....	627
TTH PRO	A..A.....	630
MAJORITY		IRVFQEGRDIHTQTASWMTGPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAI PYEEAVAFIERYFO	
TAQ PRO	E.....R.....G.....Q.....	698
TFL PRO	S..G.....G..S.....	697
TTH PRO	K.....V.....	700

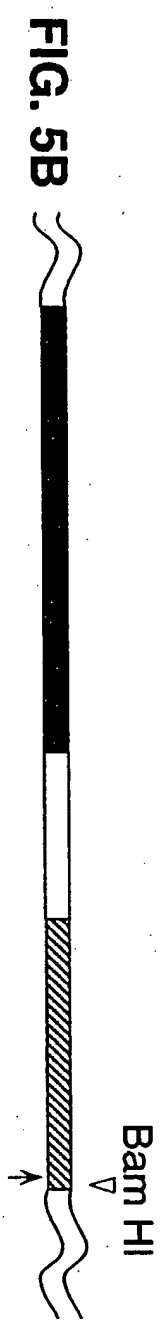
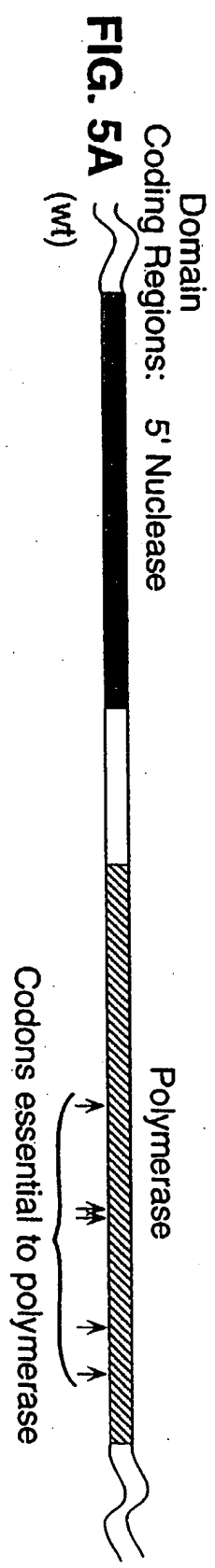
TAO PRO	[SEQ ID NO:4]	E	768
TFL PRO	[SEQ ID NO:5]	G	767
TTR PRO	[SEQ ID NO:6]	K	770

[illegible]

Genes for Wild-Type and Pol(-)DNAPTaq



Genes for Wild-Type and Pol(-) DNAPTII



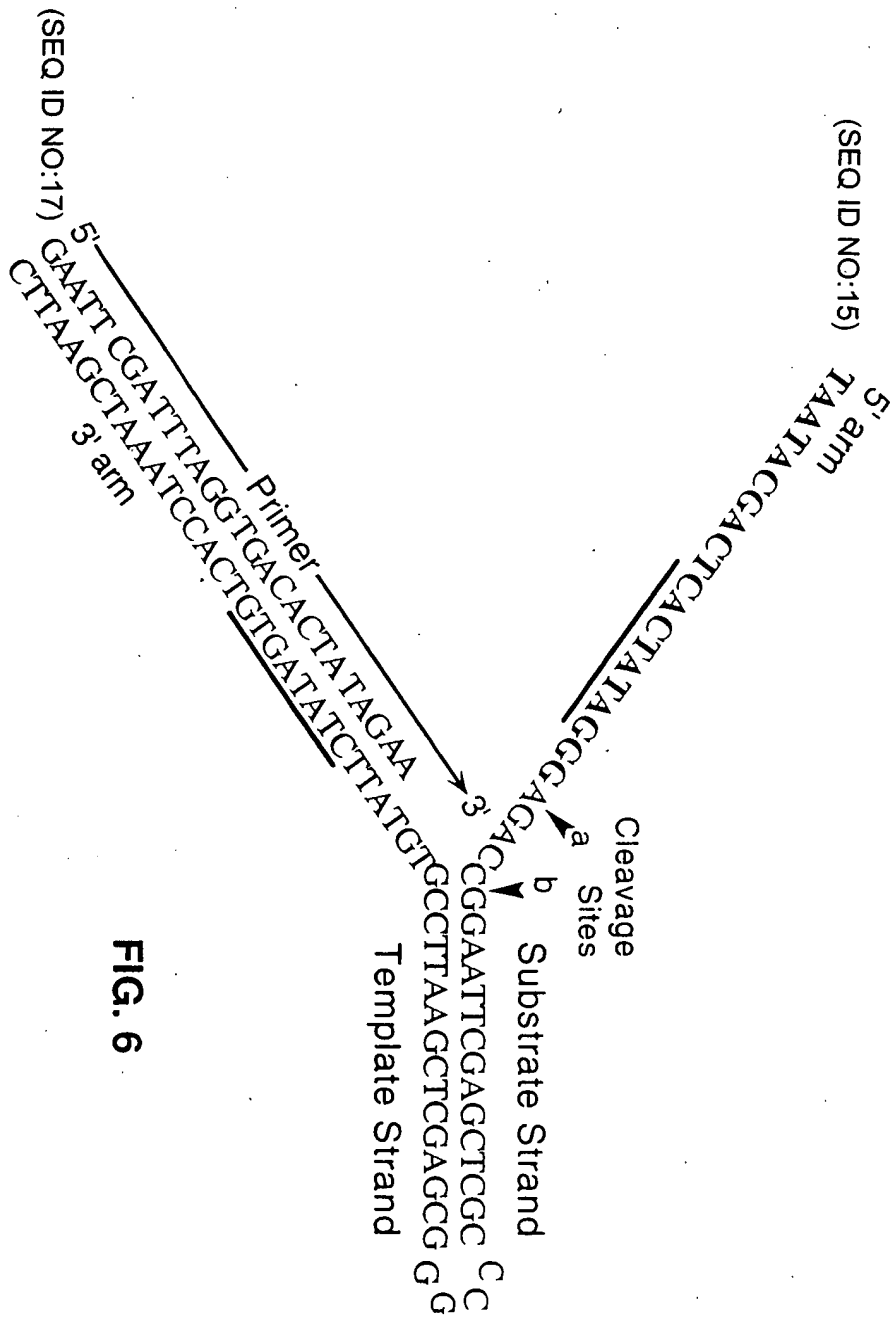


FIG. 6

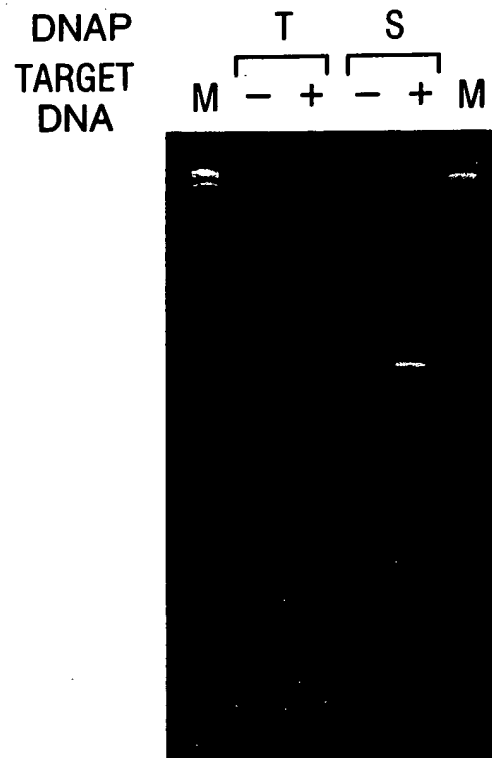


FIG. 7

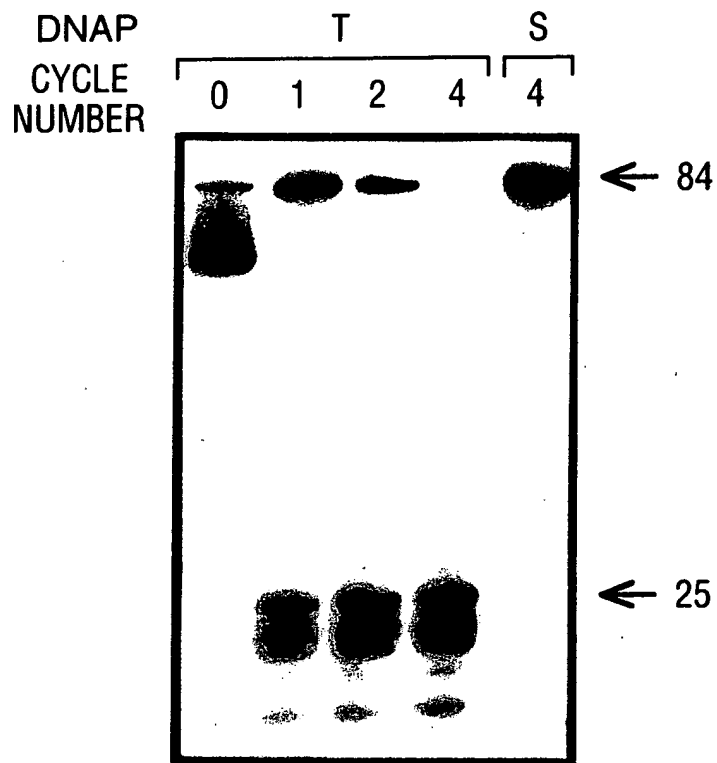


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

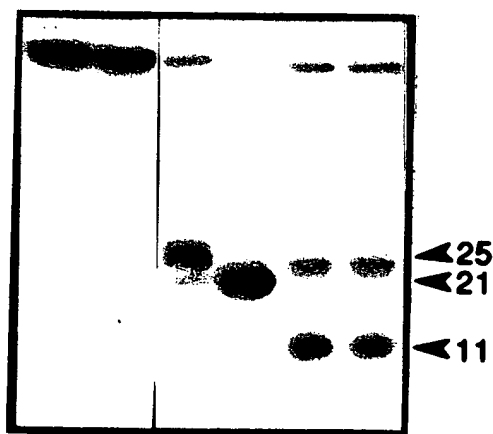


FIG. 9A

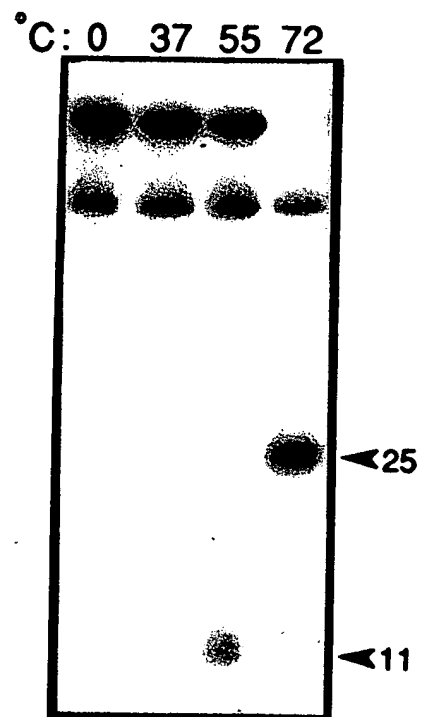


FIG. 9B

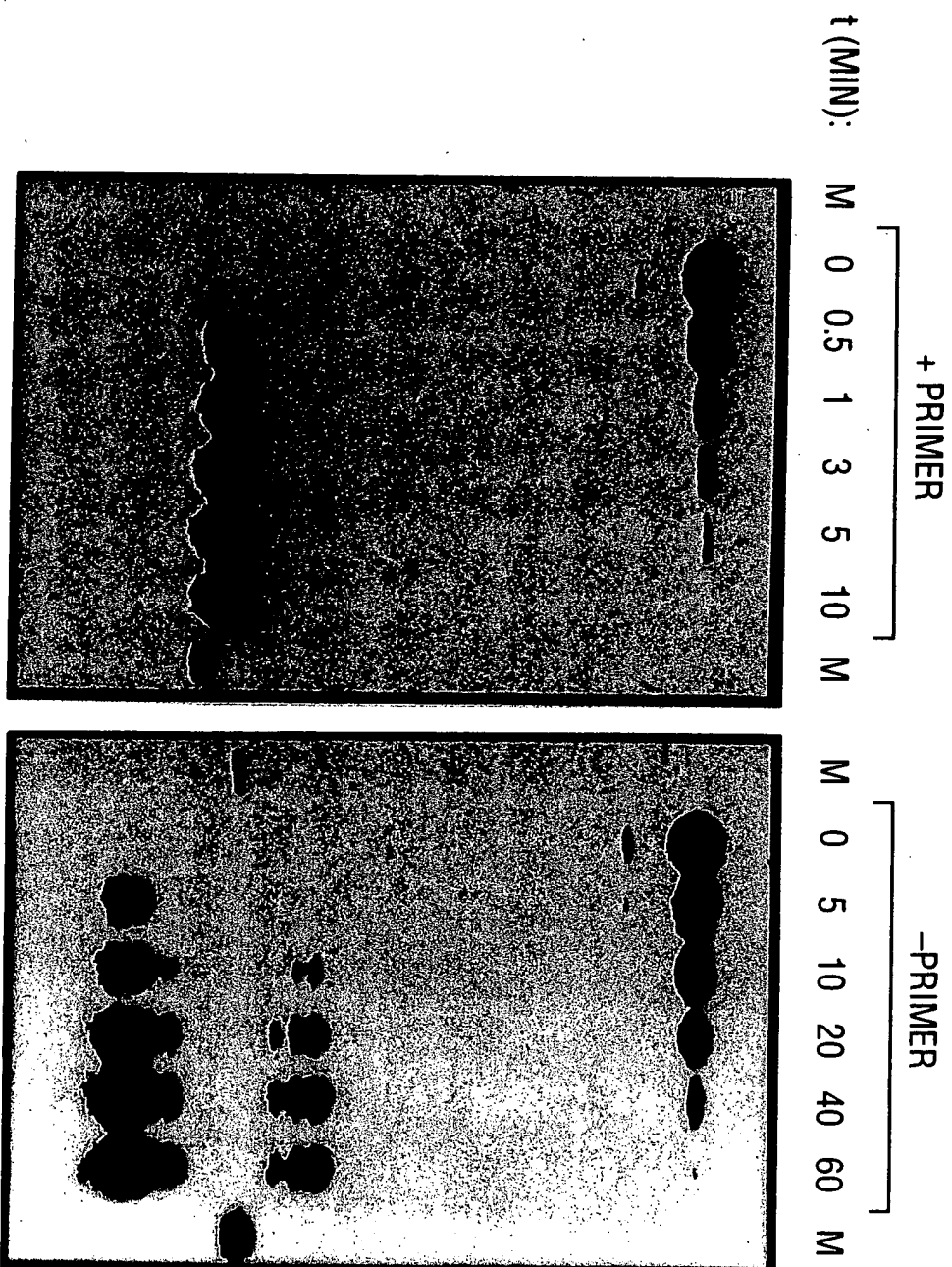


FIG. 10A

FIG. 10B

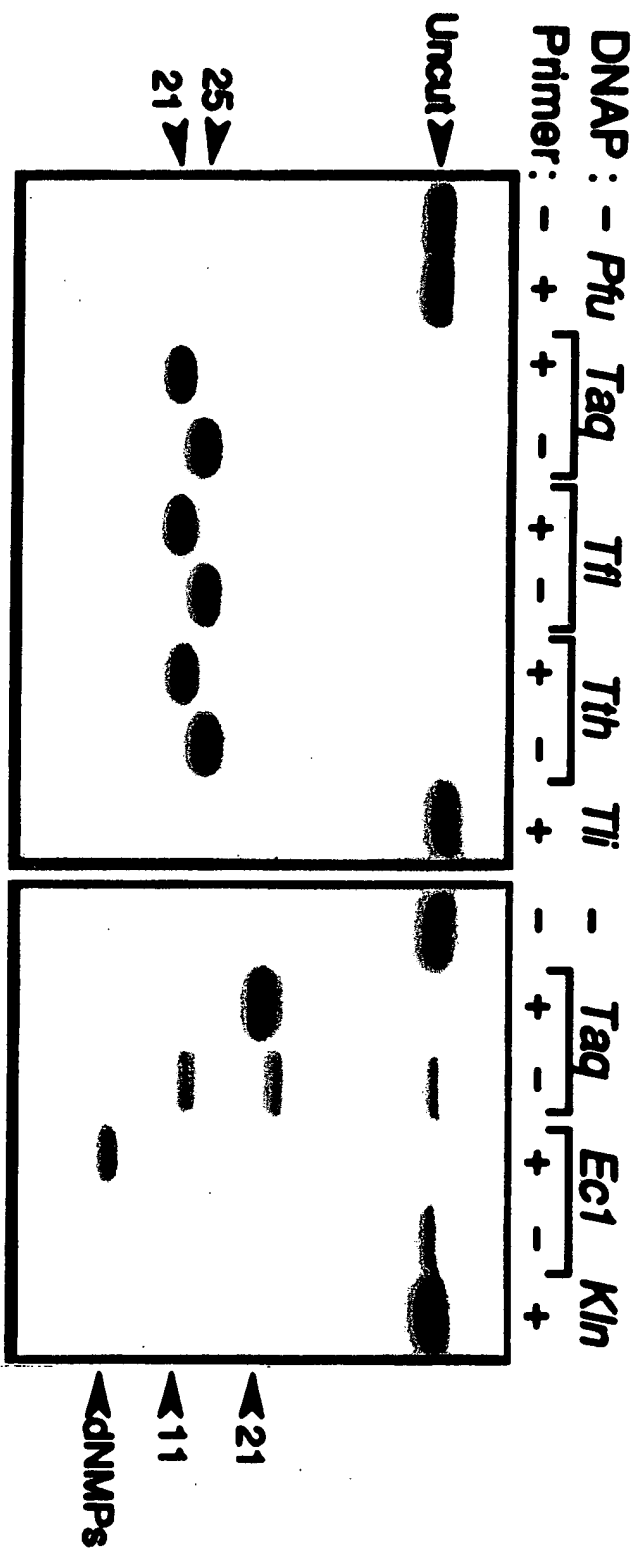
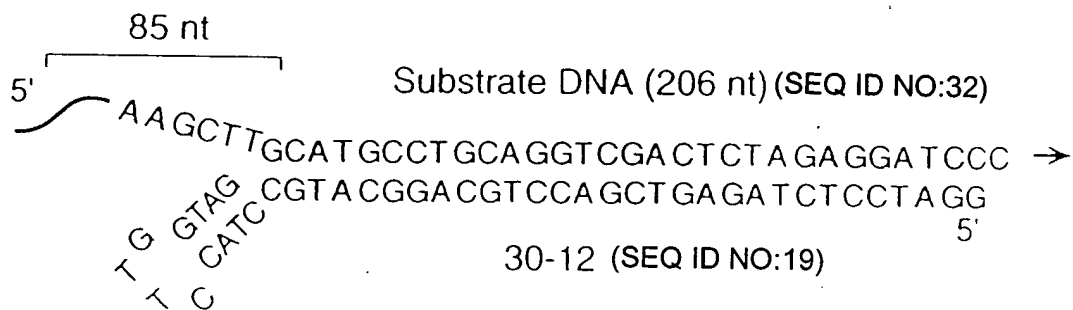
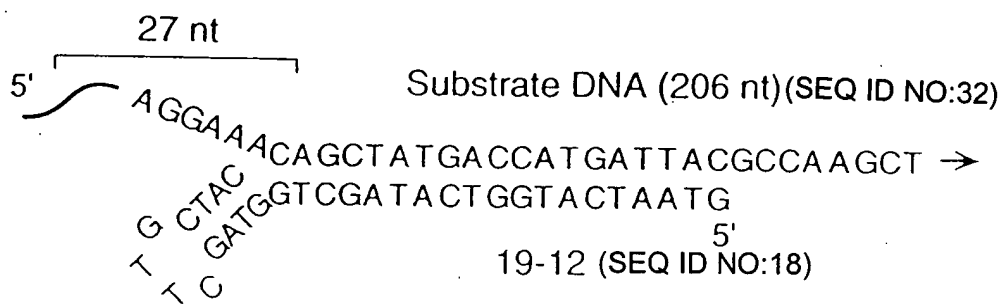


FIG. 11A

FIG. 11B

FIG. 12A



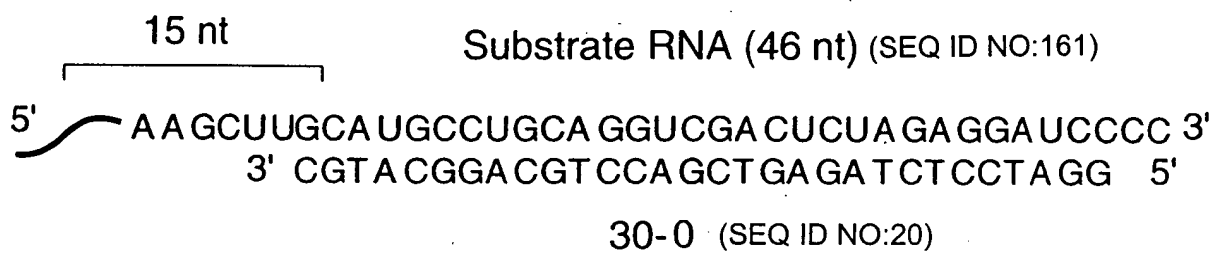


FIG. 13A

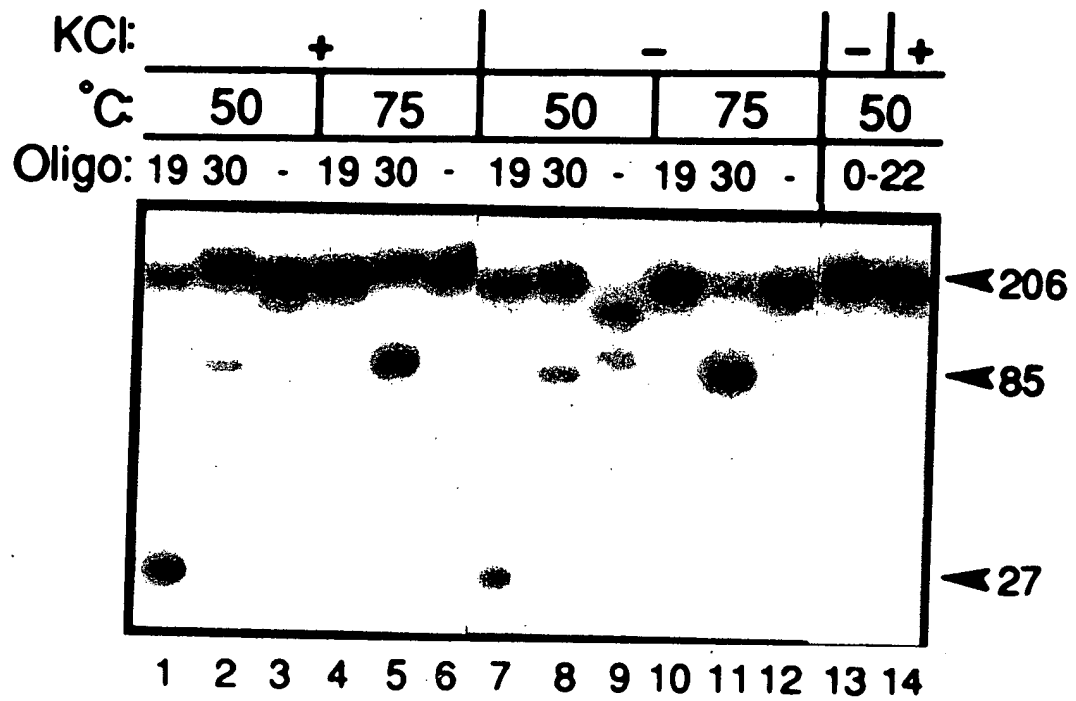


FIG. 12B

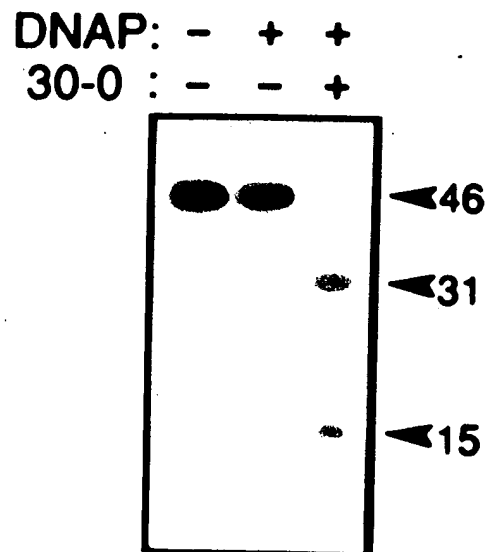


FIG. 13B

FIG. 14B

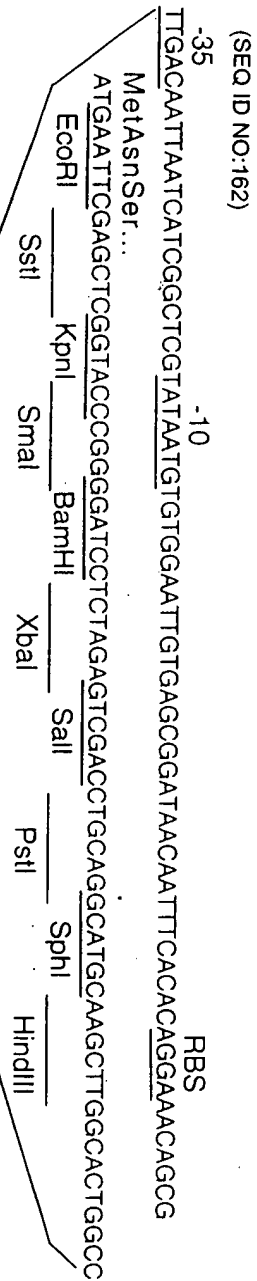


FIG. 14A

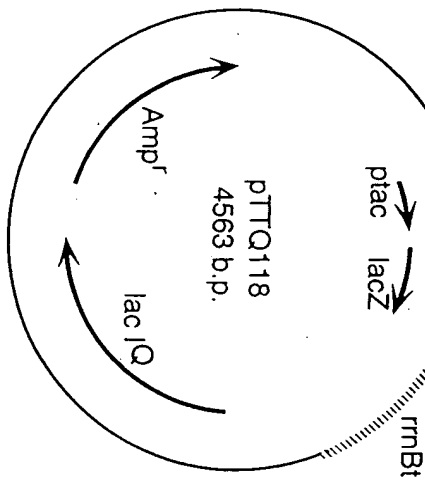


FIG. 14C

RBS: Ribosome binding site
ptac: Synthetic tac promoter
lacIQ: Lac repressor gene
lacZ: Beta-galactosidase alpha fragment
rmBt: E. coli rrmB transcription terminator

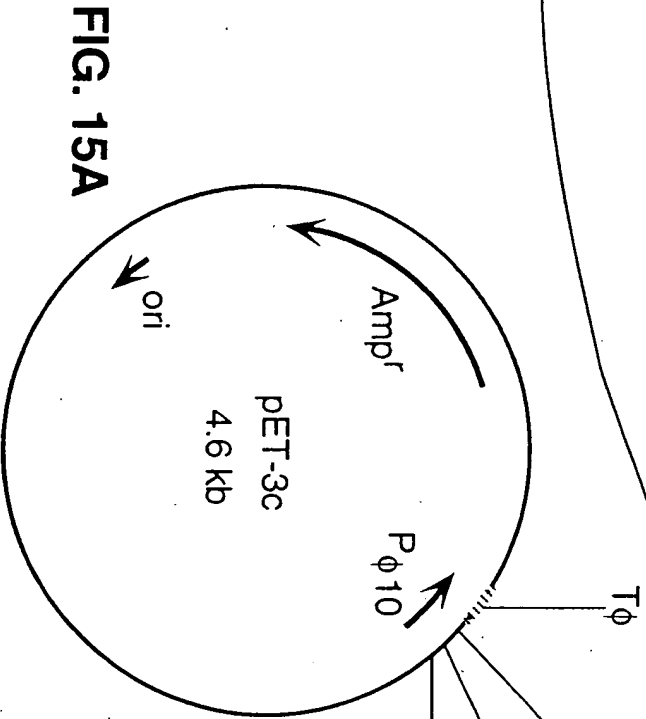
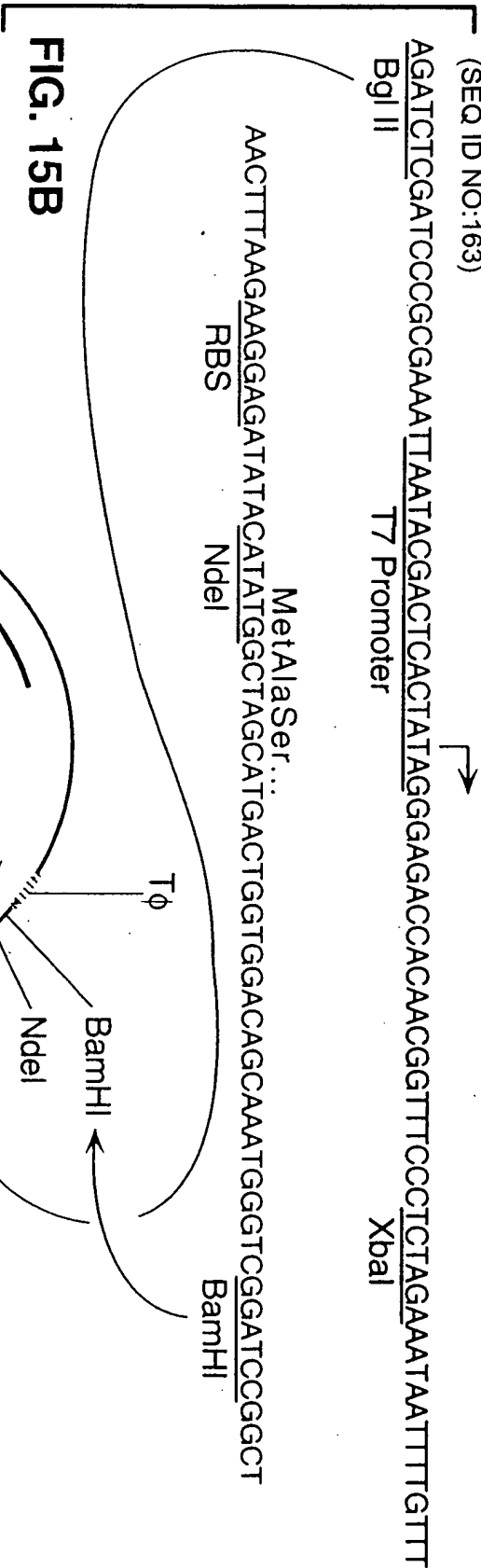


FIG. 15C

P ϕ 10: Bacteriophage T7 ϕ 10 promoter
T ϕ : T7 ϕ Terminator
RBS: Ribosome binding site

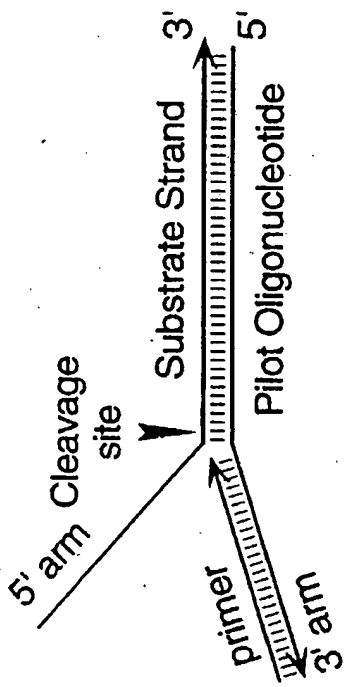


FIG. 16B

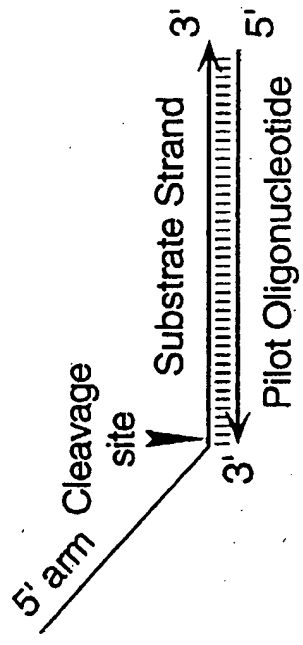


FIG. 16D

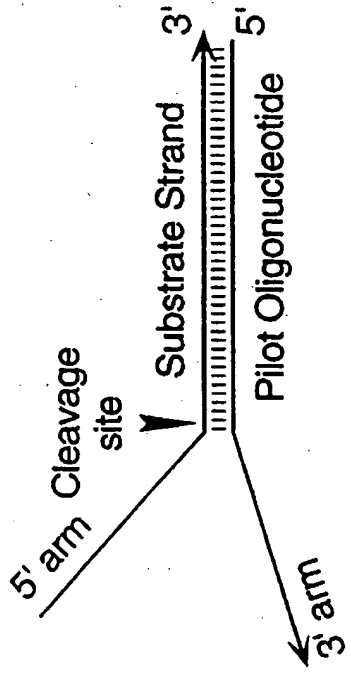


FIG. 16A

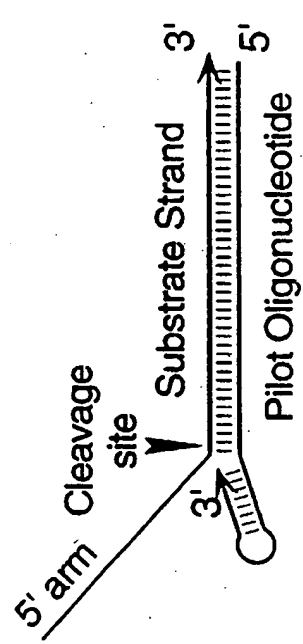


FIG. 16C

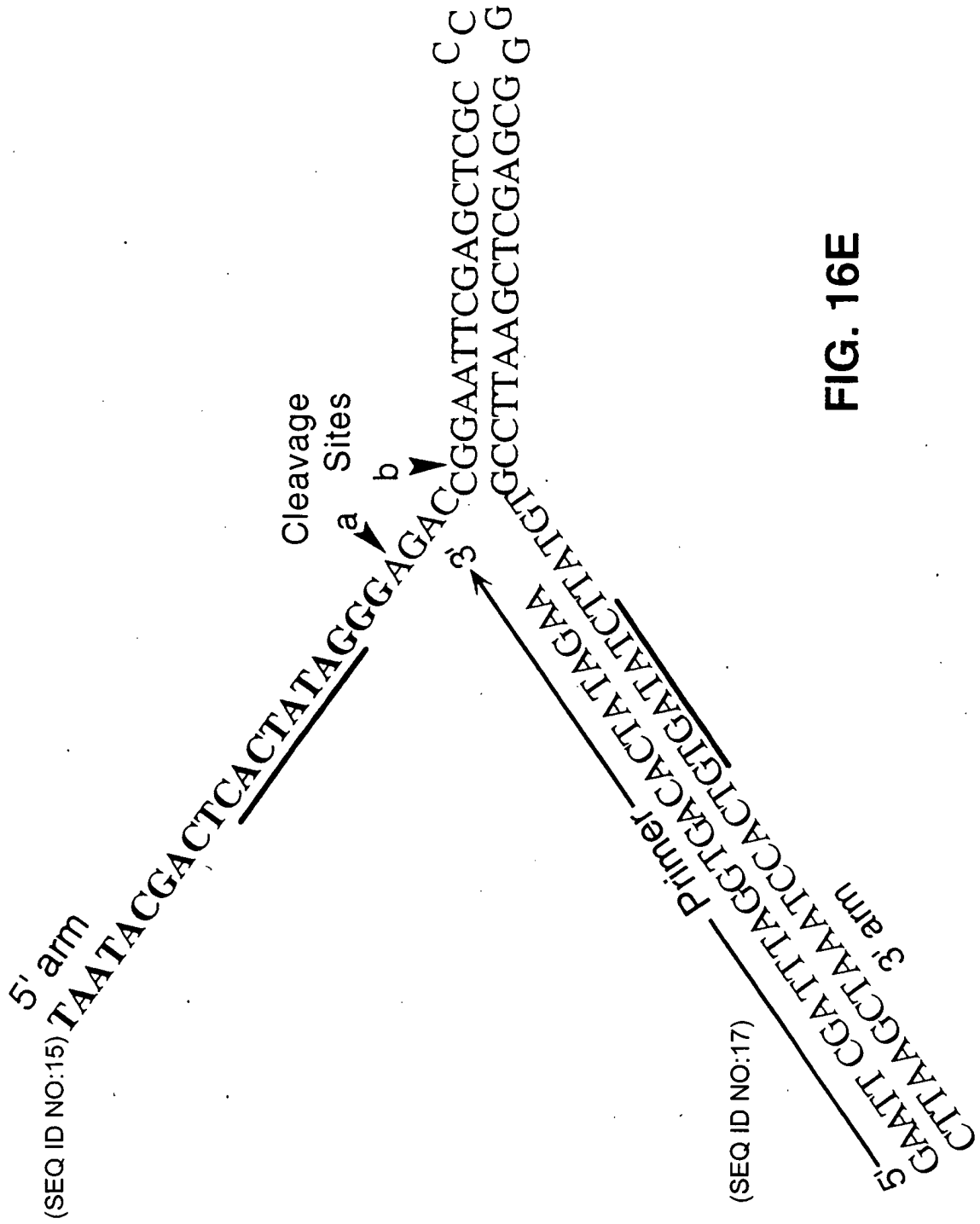
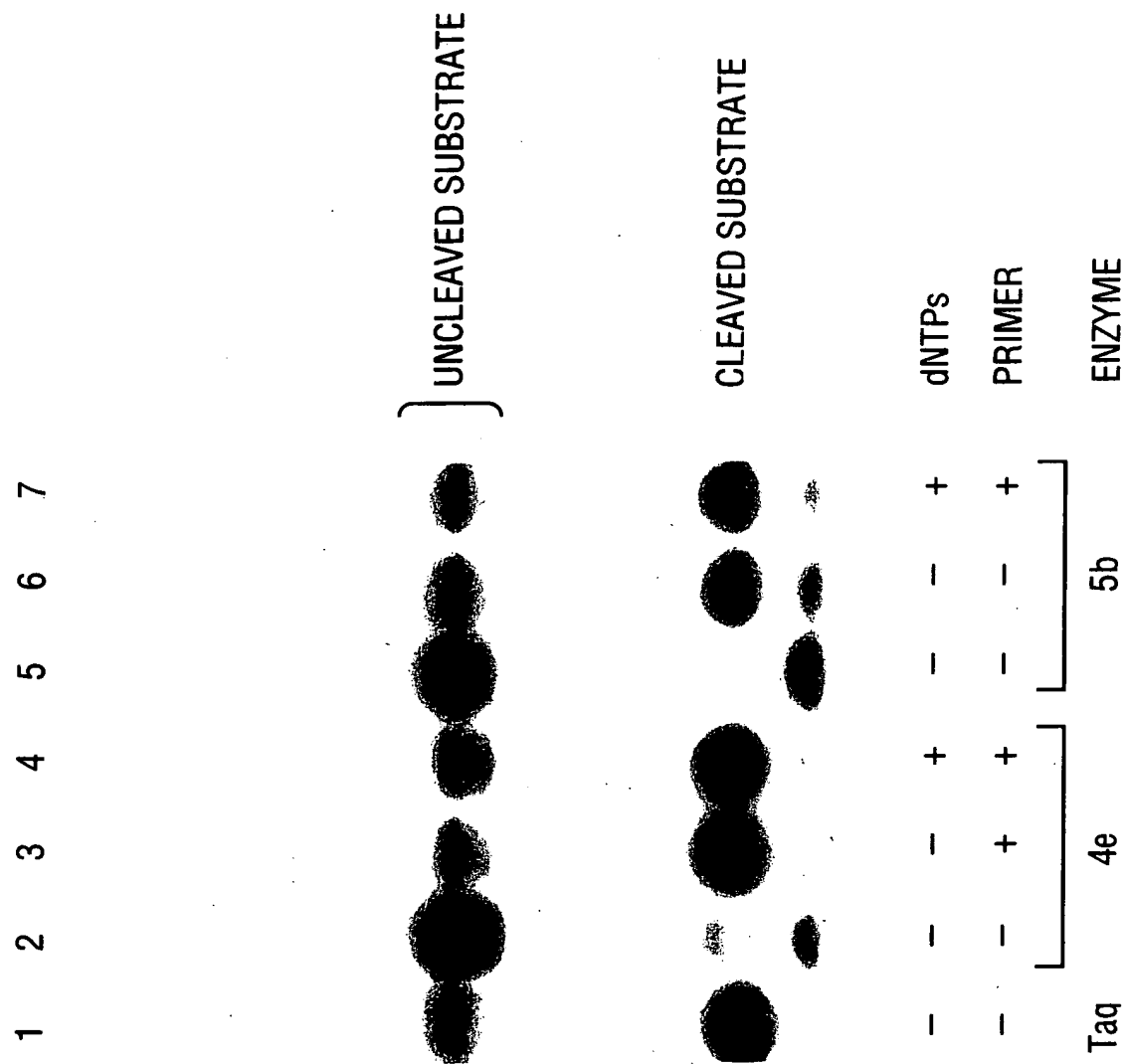


FIG. 16E



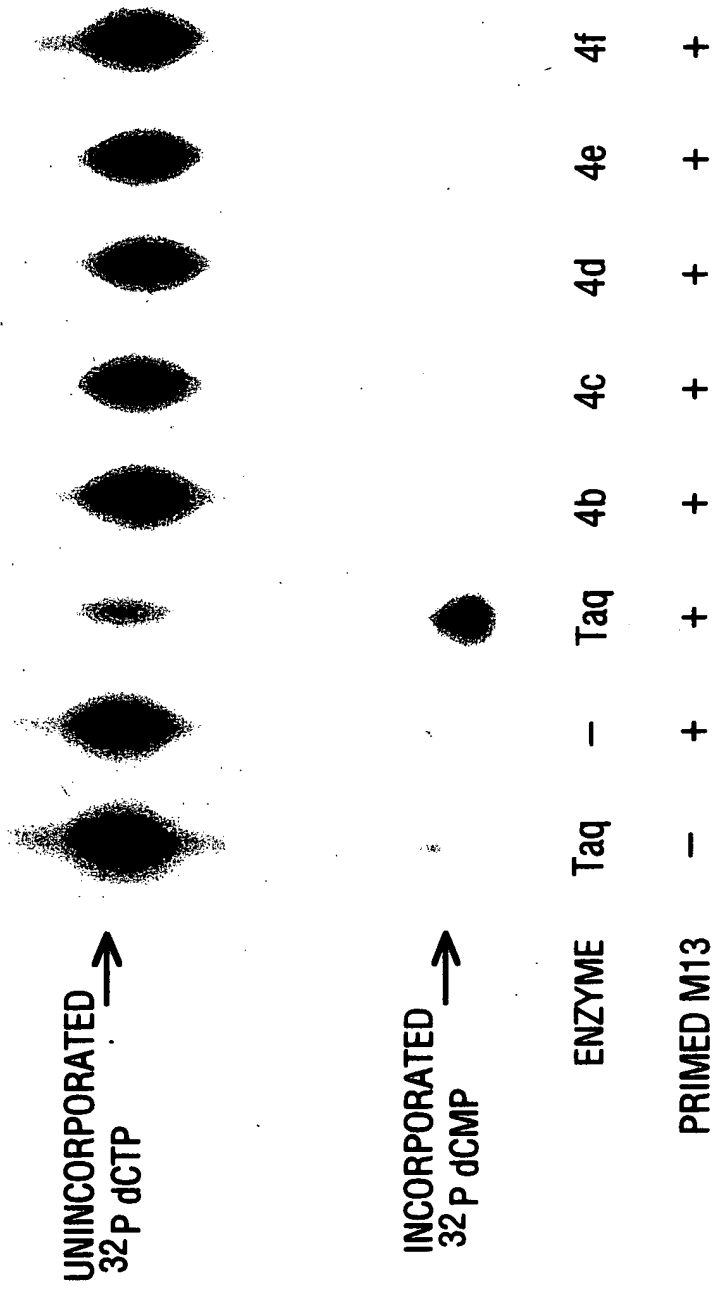


FIG. 18

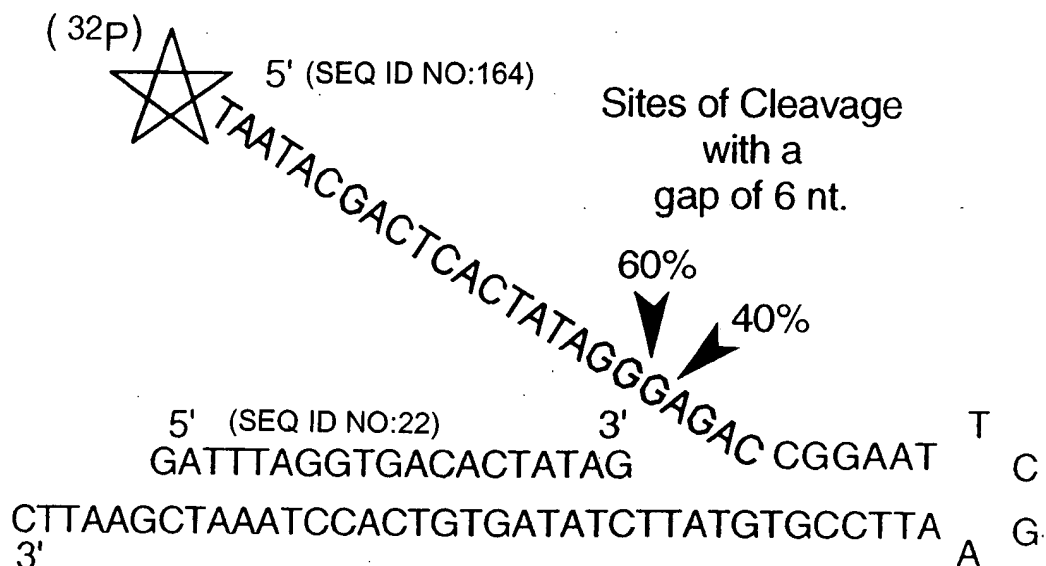


FIG. 19A

1	2	"4d"		"4b"		UNMODIFIED		dNTP
		NO POL. ACTIVITY		2 PT. MUTATION SMALL ACTIVITY		DNAP Taq		
		3	4	5	6	7	8	
		-	+	-	+	-	+	

84 NUC. —

HAIRPIN TEST MODULE

CONVERSION TO DOUBLE STRANDED
(COMPLETE EXTENSION OF PRIMER)

DESIRED PRODUCT —> 21 NUC.

MULTIPLE BANDS
CAUSED BY POLYMERIZATION

FIG. 19B

SOME ABERRANT CLEAVAGE WITH "4b"
BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

A-Hairpin
 (SEQ ID NO:23)
 Predicted
 cleavage site
 5' CGGACGAACAAGCAGACAGCAGGACACAG 3' A C
 5' Tau primer 3' GTACC CATGG T A
 3' CAAAGACGACACAGCAGACAGAGAAGCAGAA

T-Hairpin
 (SEQ ID NO:24)
 Predicted
 cleavage site
 5' GTTCTGCTGTGTGCTCTCTCTCTCTCTT 3' A T
 5' Alpha primer 3' GTACC CATGG T G
 3' CTGCTGTTCGCTCTGTGCTGTGTC

FIG. 20A

Sequence of alpha primer: (SEQ ID NO:25)
5' GACGAACAAGCGAGACAGCG 3'

FIG. 20B

5' ACACAG GTACC A C
3' CAAAGACGACACAGACGAGAGAGAGAGAA
Cleaved A-Hairpin

5' CCTCTT GTACC A T
3' CTGCTGTTGCTCTGTCGCTGTGTC
Cleaved T-Hairpin

FIG. 20C

(SEQ ID NO:28) $\text{NiAlII}^{\text{I}} \text{HgICl}$ (SEQ ID NO:27)

(SEQ ID NO:27)

5' GTTTCGTGTCGTCTCTCTTGGCCCTTTGACCATGTGGTACCTGTGTGCGTCTGCGCTTGTC
3' CAAGAGCAGACACAGCAGAGAACGAGAACATGTGTACCATGTGACACAGCGACAGAGCGAACACAGCGGC 5'

Restriction sites: BsmAI, MnlI, RsaI, KpnI, BsmAI

(SEQ ID NO:24)

T-Hairpin
A-Hairpin
(SEQ ID NO:23)

FIG. 20D

(SEQ ID NO:23)

ECOR. 1

7-1101 30-0

↑
[]

206

FIG. 21

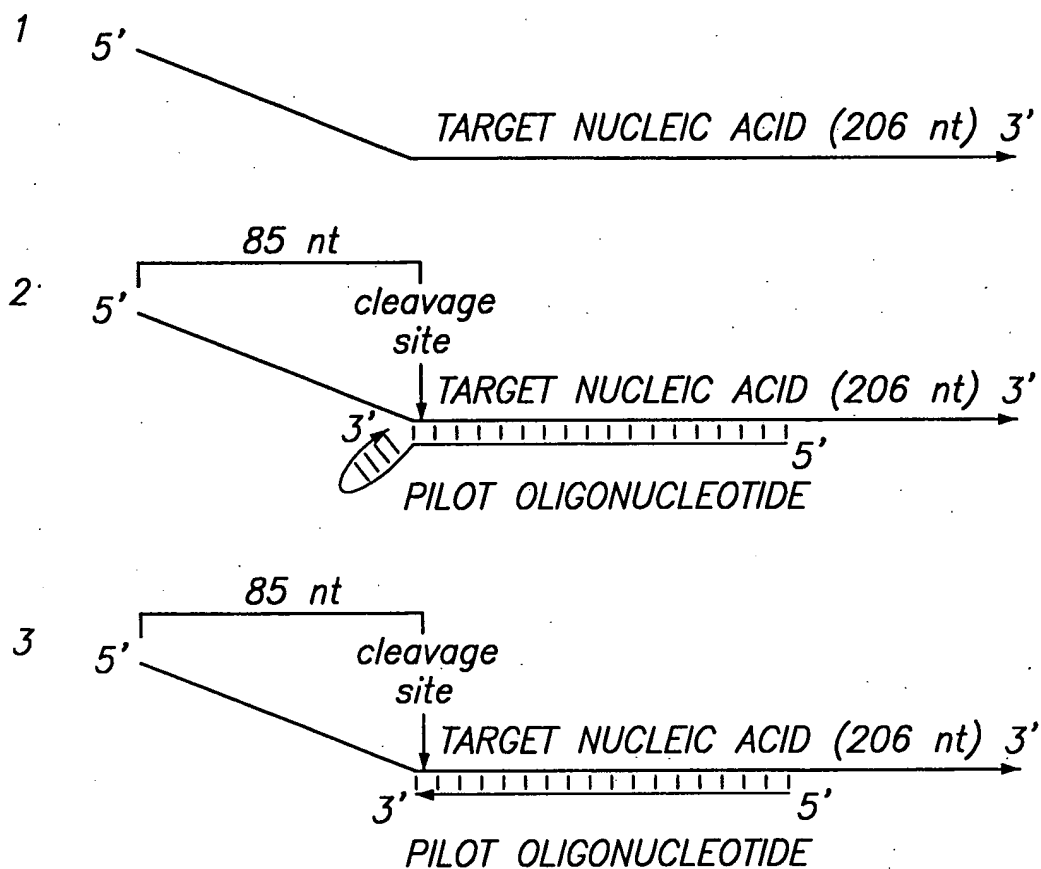


FIG. 22A

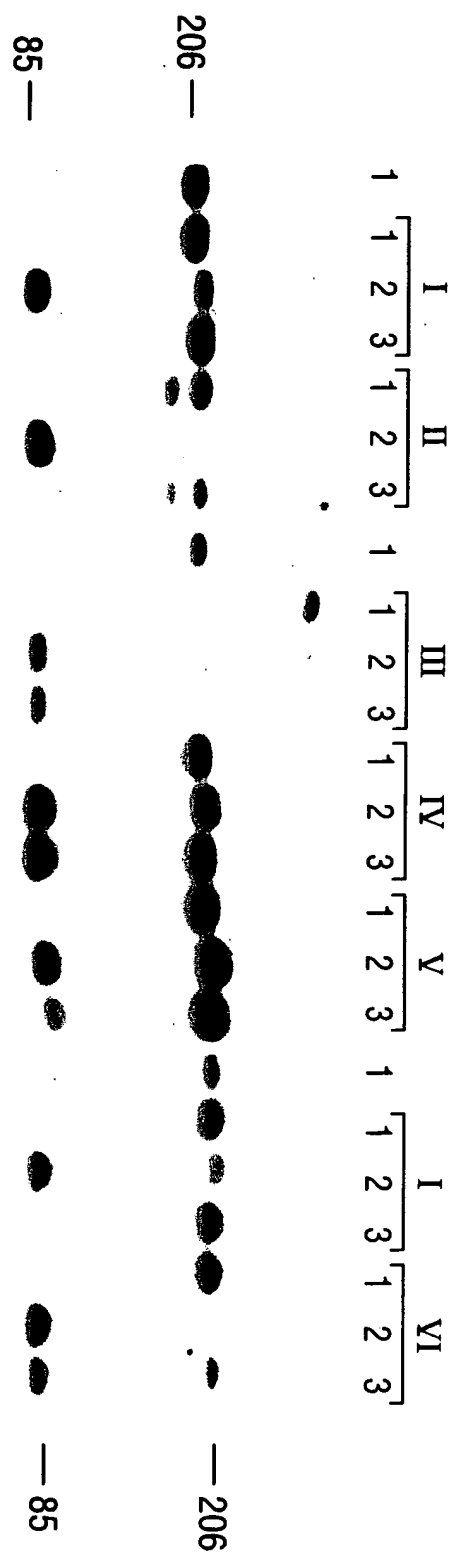


FIG. 22B

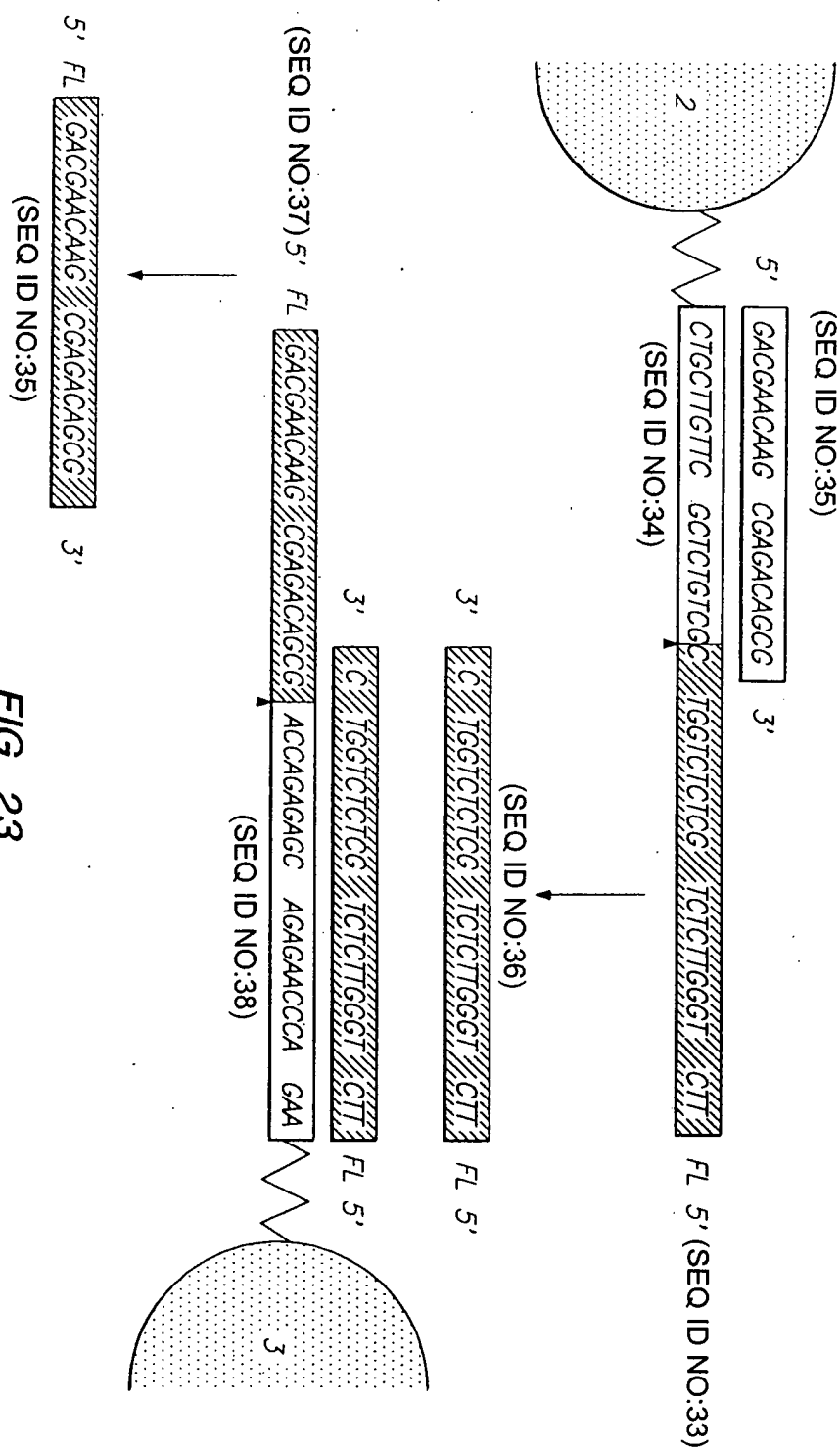


FIG. 23

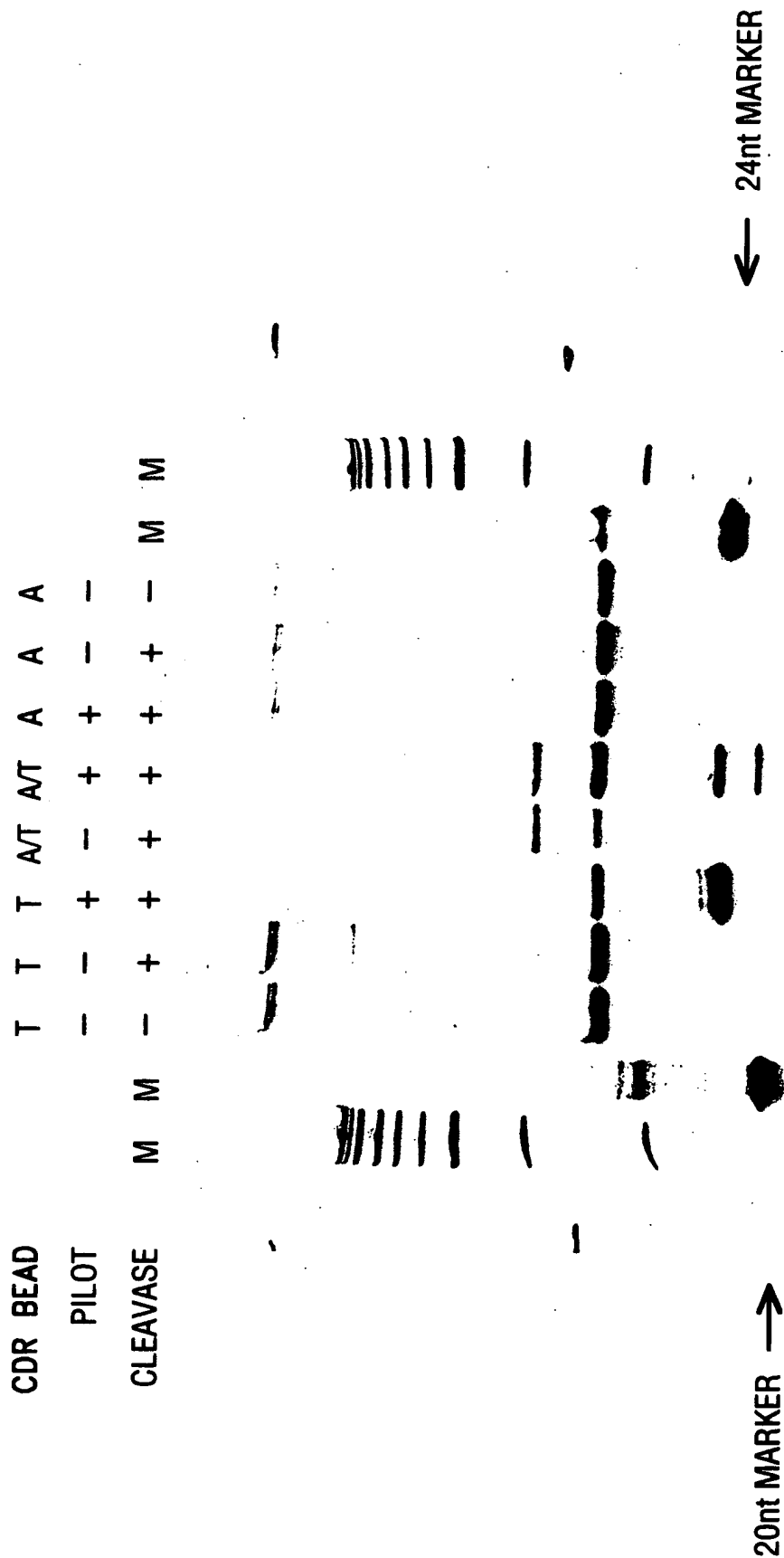


FIG. 24

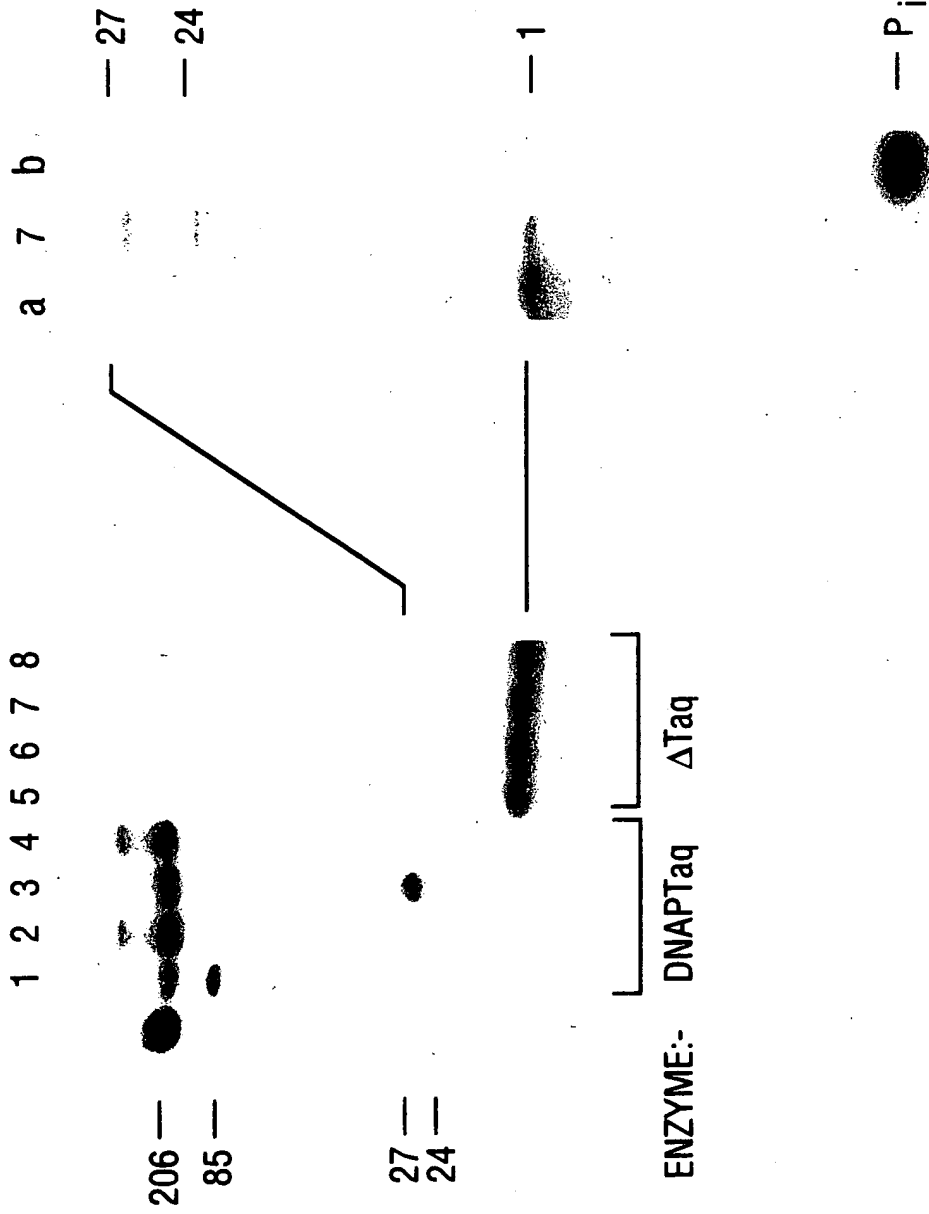


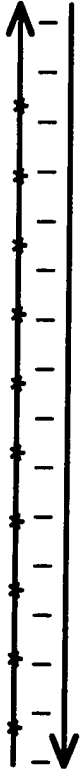
FIG. 25B

FIG. 25A

FIG. 26A



FIG. 26B



* = 32p



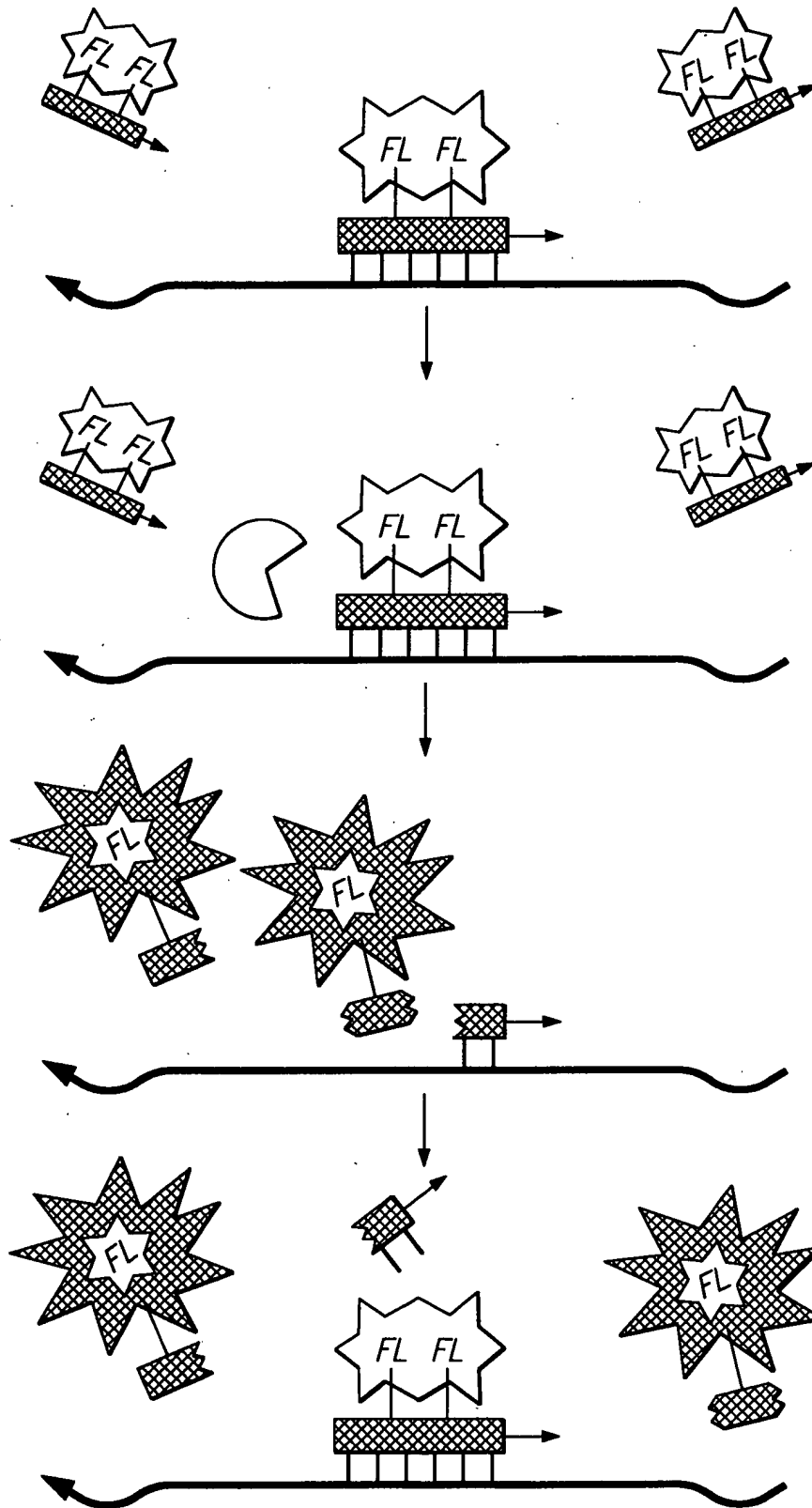


FIG. 27

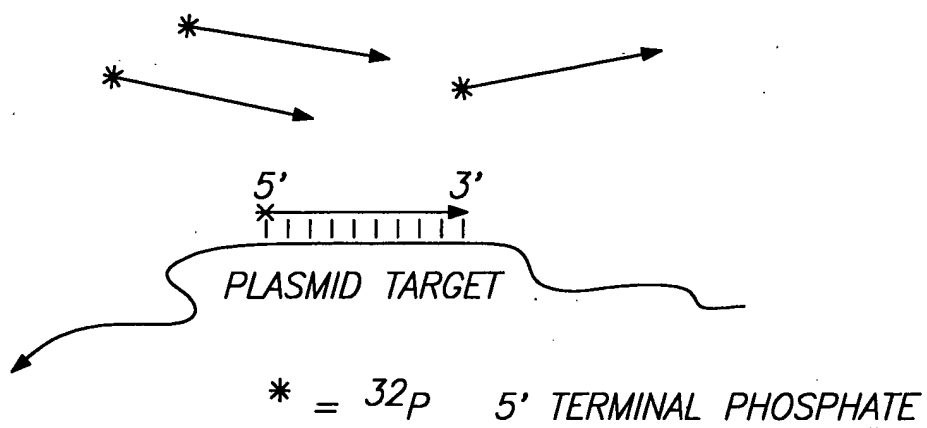


FIG. 28A

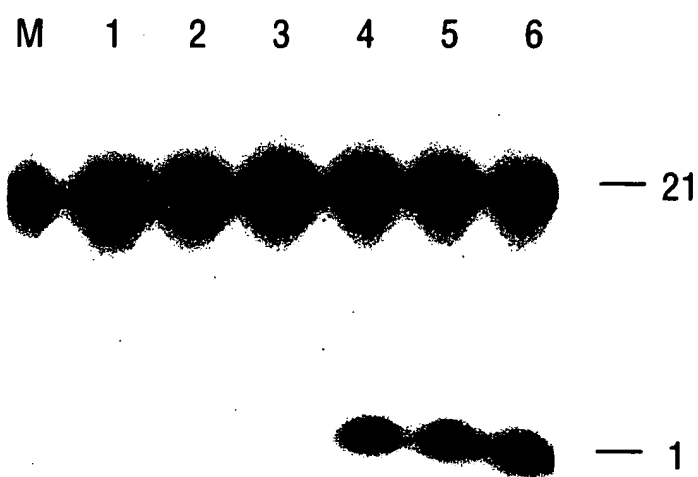


FIG. 28B

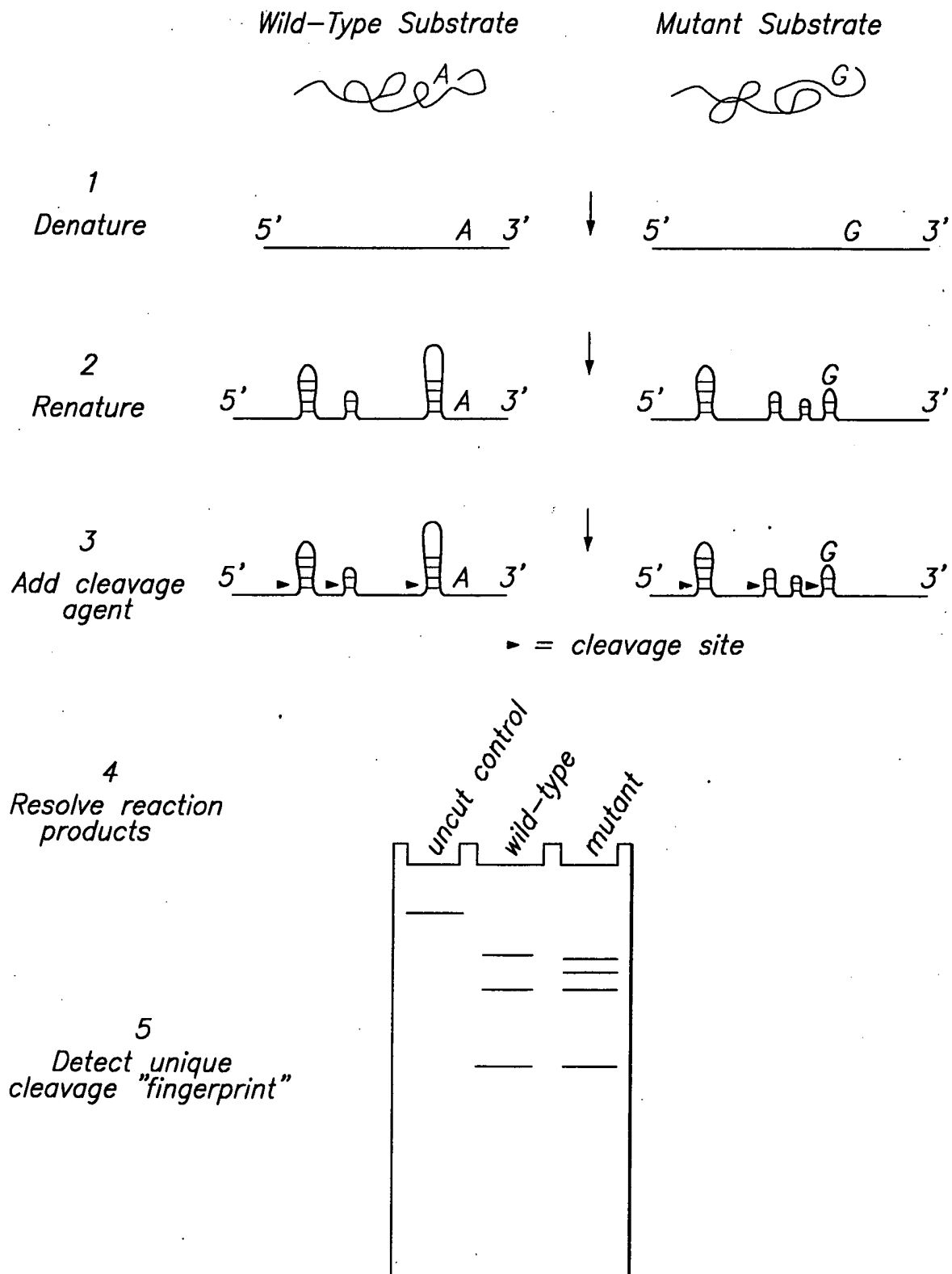


FIG. 29

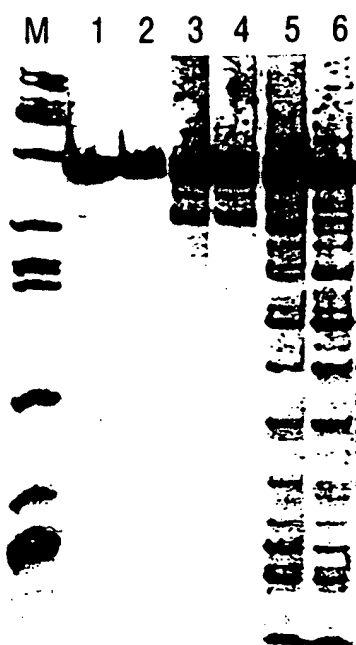


FIG. 30

1. The following information is being furnished to you for your information:

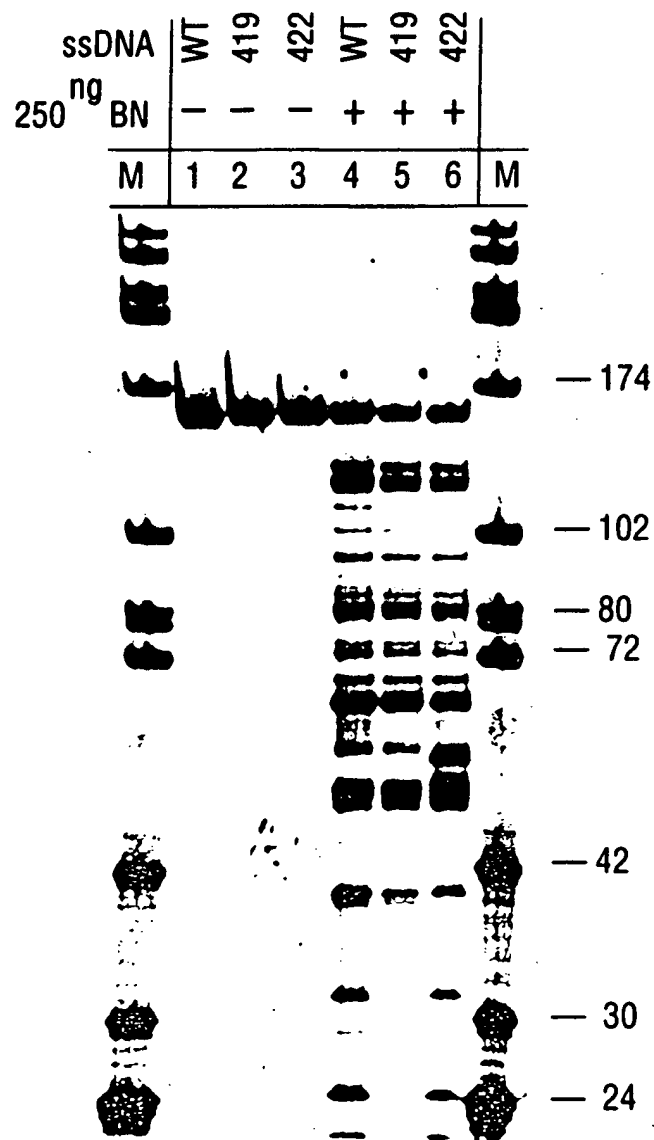


FIG. 32

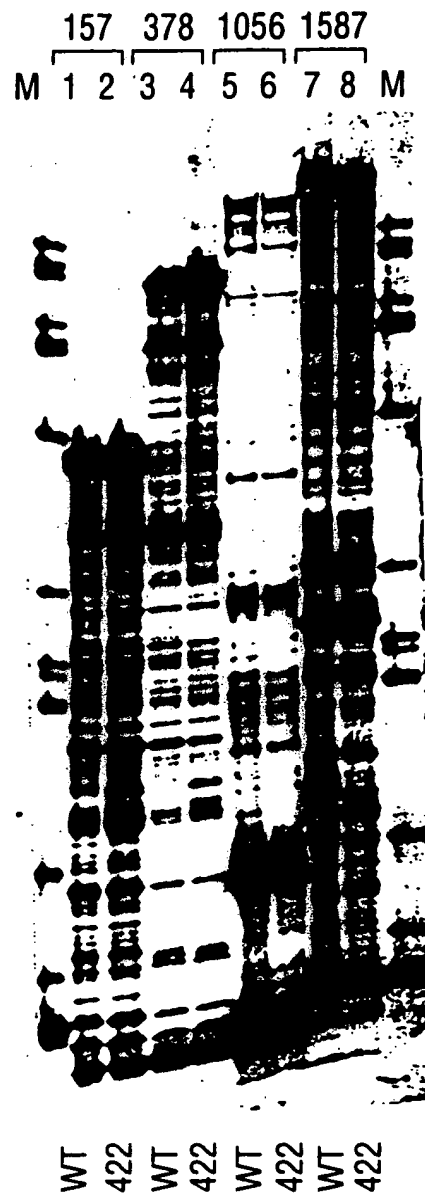


FIG. 33

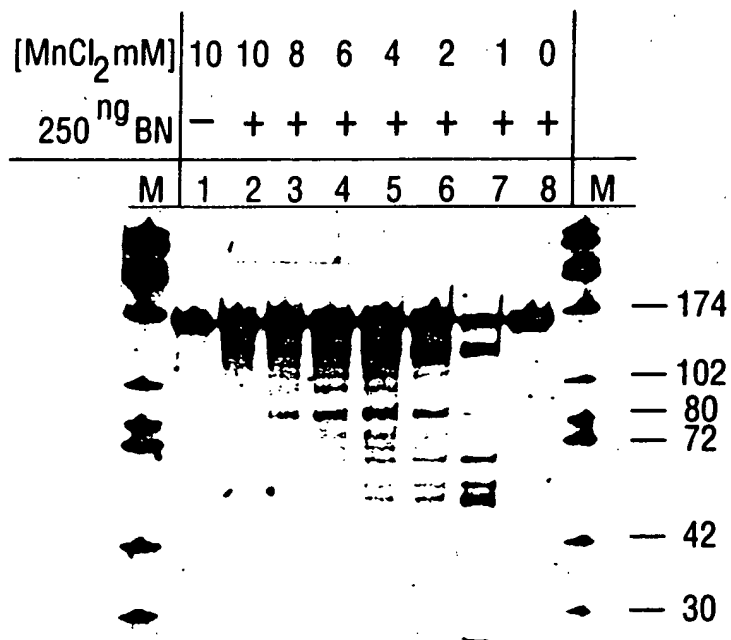


FIG. 34

FIG. 35

TIME (MIN.):	10	<.1	1	5	10
CLEAVASE™BN:	—	+	+	+	+

CLEAVASE™BN (ng): — 10 50 100 250

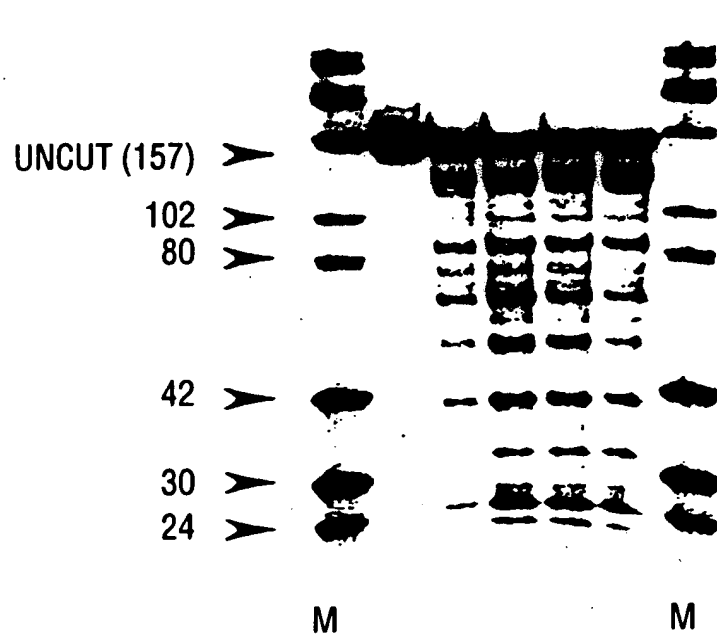


FIG. 38

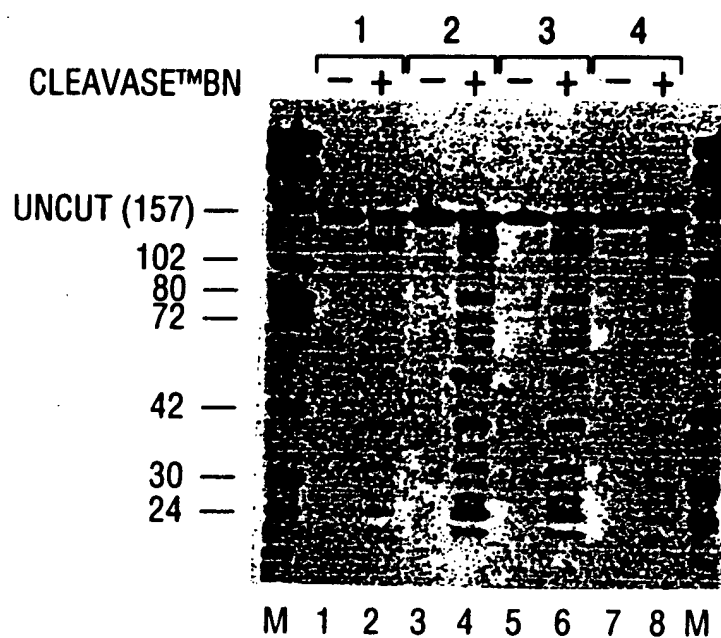


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCCEIN ANTI-SENSE STRAND					
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 ^{ng} BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

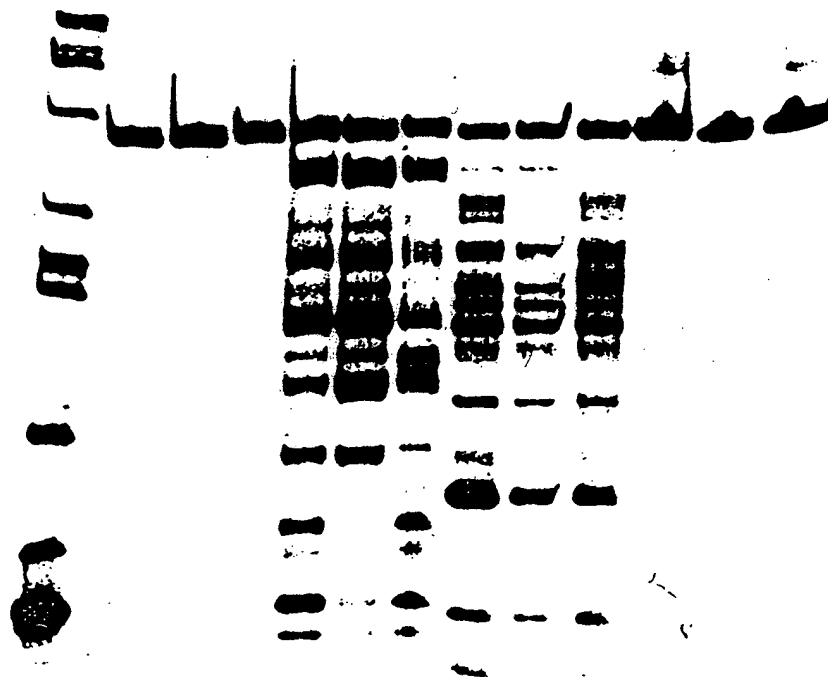


FIG. 40

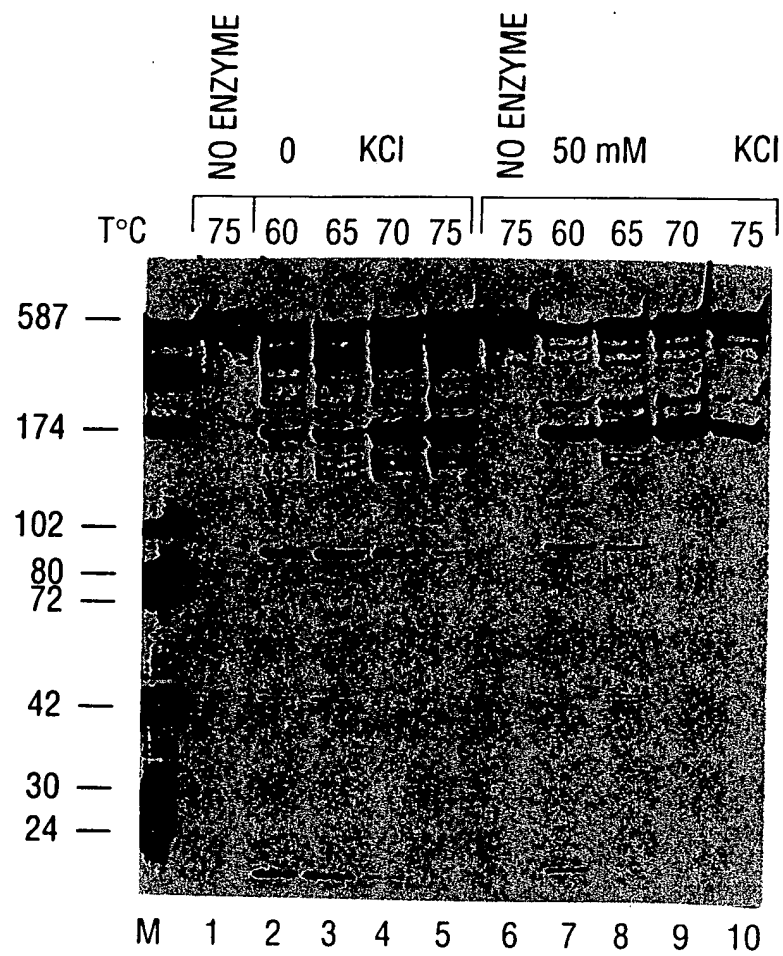


FIG. 41

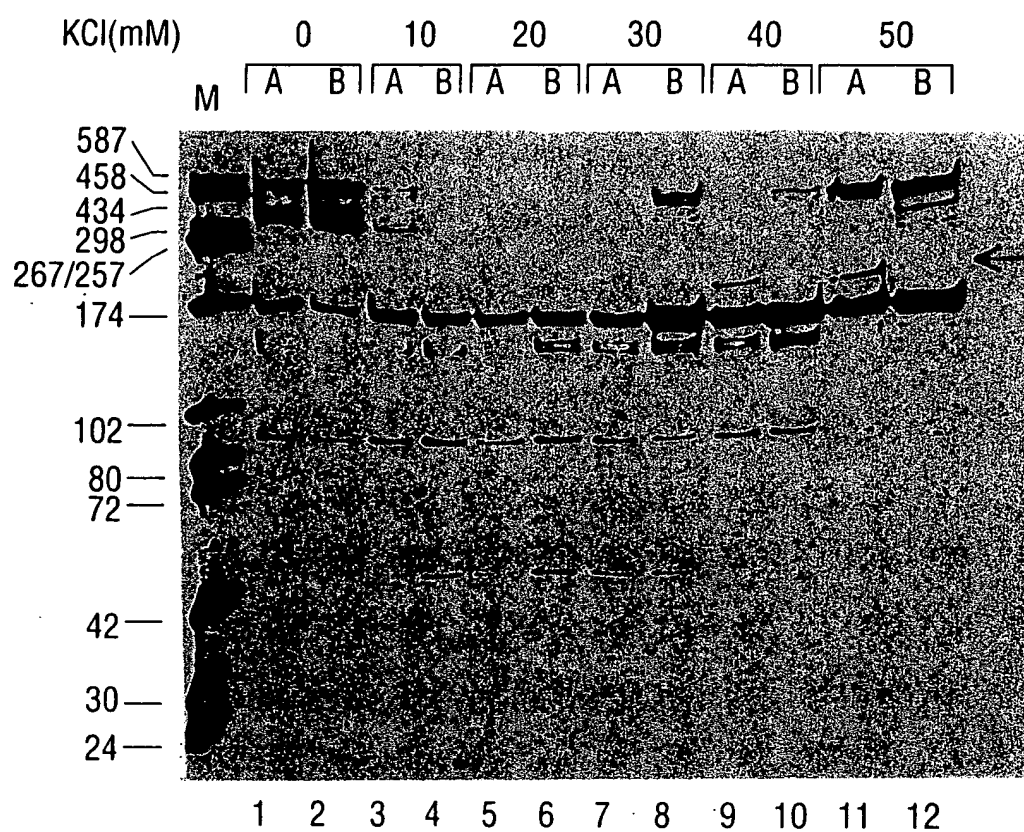


FIG. 42



FIG. 43

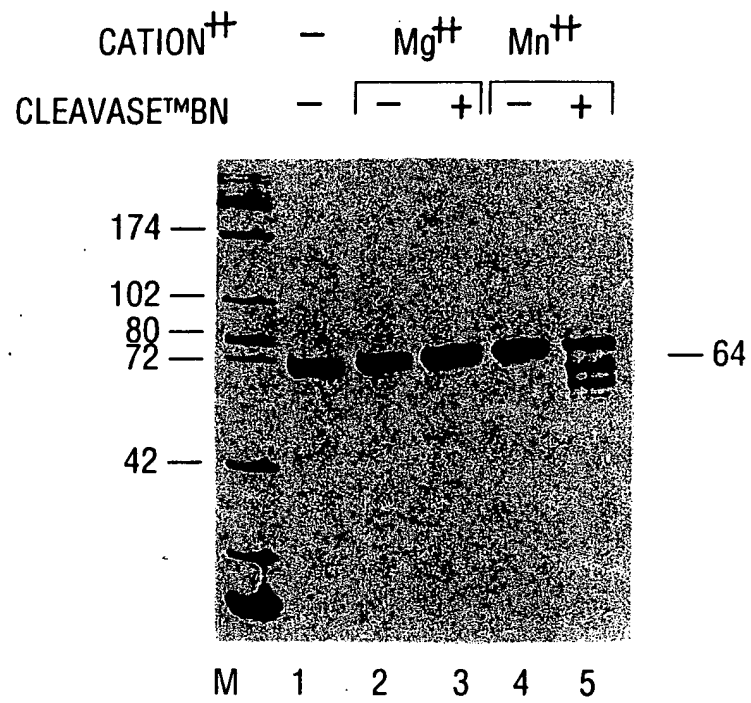


FIG. 44

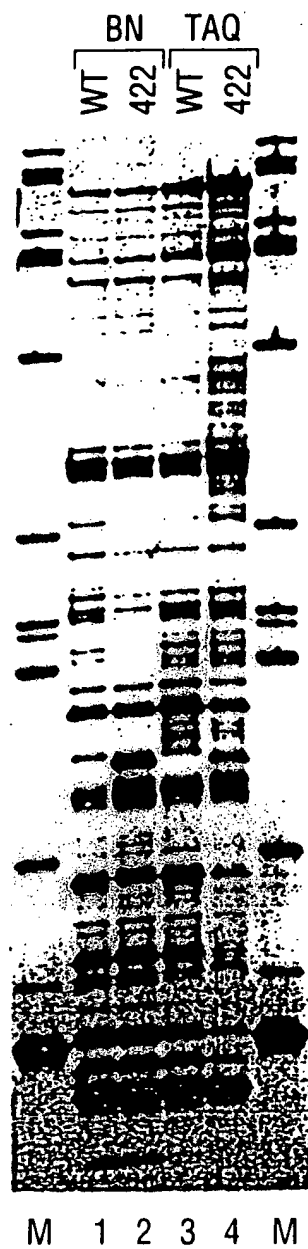


FIG. 45

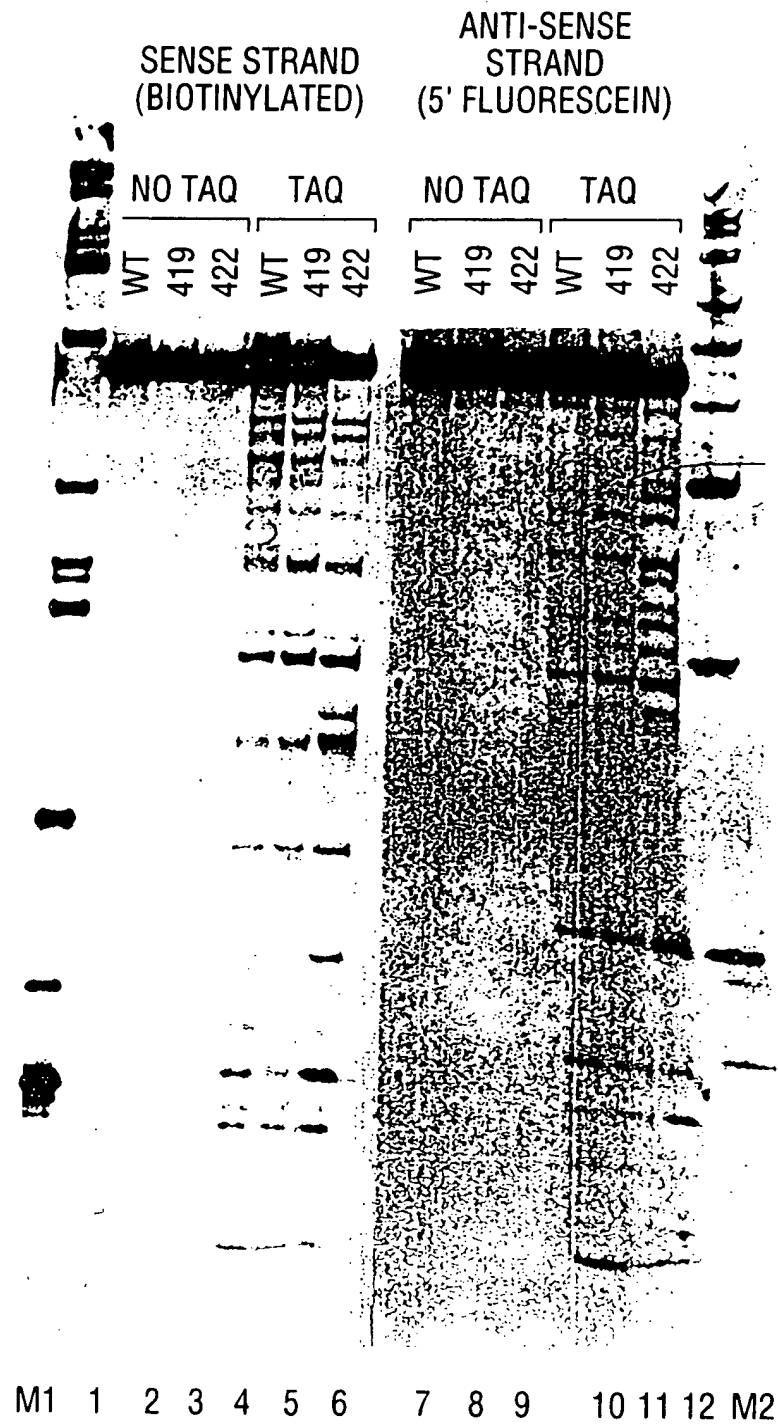


FIG. 46

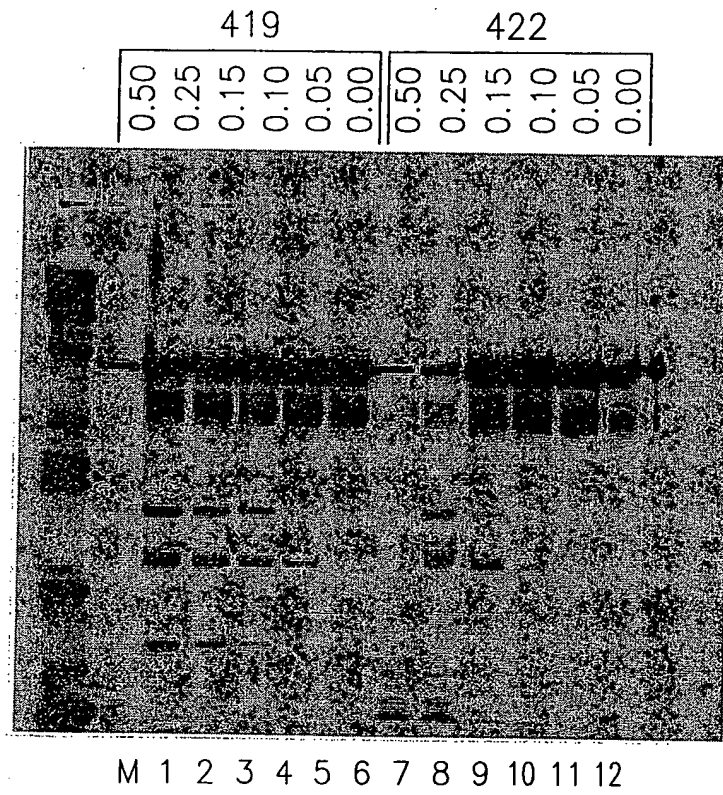


FIG. 47

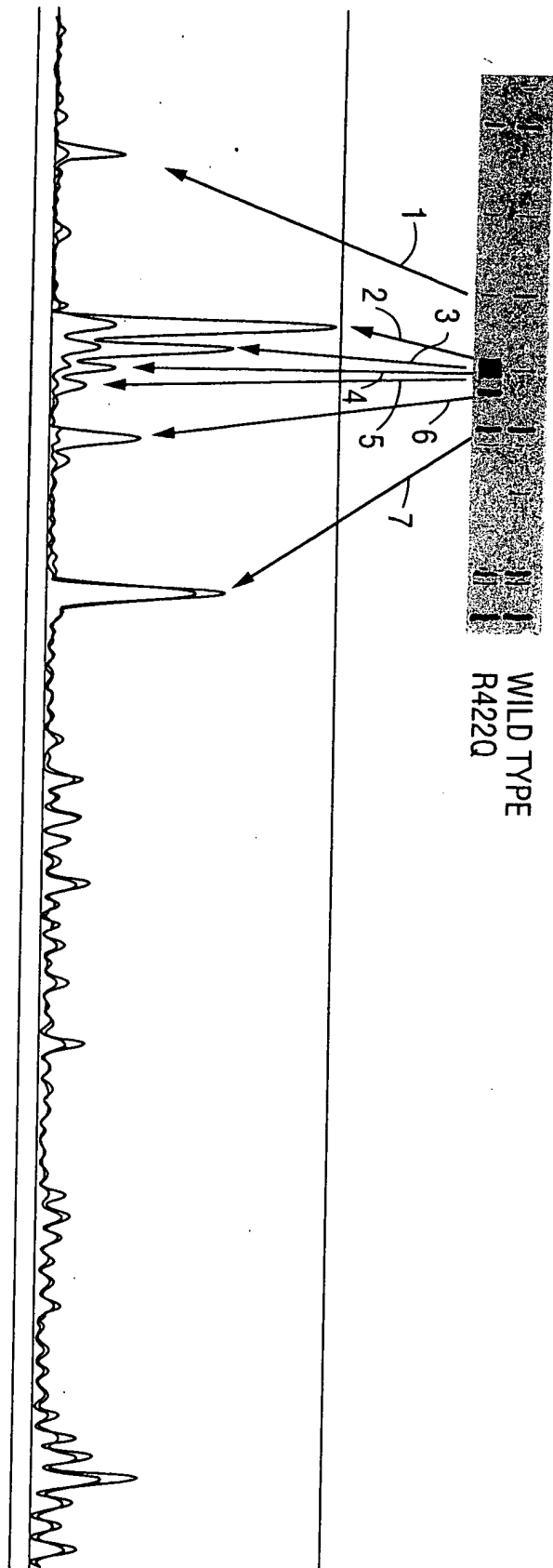


FIG. 48

L.100.8-1 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
 (SEQ ID NO: 76) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC

L.46.16-10 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
 (SEQ ID NO: 77) 3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
 (SEQ ID NO: 78) 3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
 (SEQ ID NO: 79) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC

L.CEM/251 5'GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG
 (SEQ ID NO: 80) 3'CCGACTGTTCTTCCTTTGAGCGACTTTGTCTCCCTGAAAGGTGTTCCCC

L.36.8-3 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
 (SEQ ID NO: 81) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC

FIG. 49A

L.100.8-1	100	ATGTTACGGGAGGTACTGGGAGGAGCCGGTCGGGAACGCCCACTCTCT
(SEQ ID NO: 76)		TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGTGAGAGA
L.46.16-10		ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT
(SEQ ID NO: 77)		TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA
L.46.16-12		ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT
(SEQ ID NO: 78)		TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA
L19.16-3		ATGTTACGGGAGGTACTGGGAGGAGCCGGTCGGGAACGCCCTCTCT
(SEQ ID NO: 19)		TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGAGAGA
L.CEM/251		ATGTTACGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTCT
(SEQ ID NO: 80)		TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGTGAAAGA
L.36.8-3		ATGTTACGGGAGGTACTGGGAGGAGCCGGTCGGGAACGCCCACTCTCT
(SEQ ID NO: 81)		TACAATGCCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGTGAGAGA

FIG. 49B

L.100.8-1	<div>150</div> 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L.46.16-10	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L.46.16-12	5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACCACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L.19.16-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L.CEM/251	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT
L.36.8-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT

FIG. 49C

L.100.8-1	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	200
L.46.16-10	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.46.16-12	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.19.16-3	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.CEM/251	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.36.8-3	GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC	

FIG. 49D

L. 100. 8 -1 (SEQ ID NO: 76)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAATTTCTGGAGAAGTTATTTTCGACGC	300
L. 46.16-10 (SEQ ID NO: 77)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAATTTCTGGAGAAGTTATTTTCGACGG	
L. 46.16-12 (SEQ ID NO: 78)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAATTTCTGGAGAAGTTATTTTCGACGG	
L. 19.16-3 (SEQ ID NO: 79)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAATTTCTGGAGAAGTTATTTTCGACGG	
L. CEM/251 (SEQ ID NO: 80)	CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCAGCGAGGTGCGAACGAATTTCTGGAGAAGTTATTTTCGACGG	
L. 36.8-3 (SEQ ID NO: 81)	CAGAGCGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCGCGGAGGTGCGAACGAATTTCTGGAGAAGTTATTTTCGACGG	
HAIRPIN		

FIG. 49F

L.100.8-1	5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG 3'TAAATCTTCATCCGGTCACACACAAGGGTAGAGGATCGGCGCGGAC	350 G 3' C 5'
L.46.16-10	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG 3'TAAATCTTCATTCGGTCACACACAAGGGTAGAGGATCGGCGCGGAC	G 3' C 5'
L.46.16-12	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG 3'TAAATCTTCATTCGGTCACACACAAGGGTAGAGGATCGGCGCGGAC	G 3' C 5'
L.19.16-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG 3'TAAATCTTCATCCGATCACACACAAGGGTAGAGGATCGGCGCGGAC	G 3' C 5'
L.CEM/251	5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG 3'TAAATCTTCATTCGATCACACACAAGGGTAGAGGATCGGCGCGGAC	G 3' C 5'
L.36.8-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG 3'TAAATCTTCATCCGATCACACACAAGGGTAGAGGATCGGCGCGGAC	G 3' C 5'

FIG. 49G

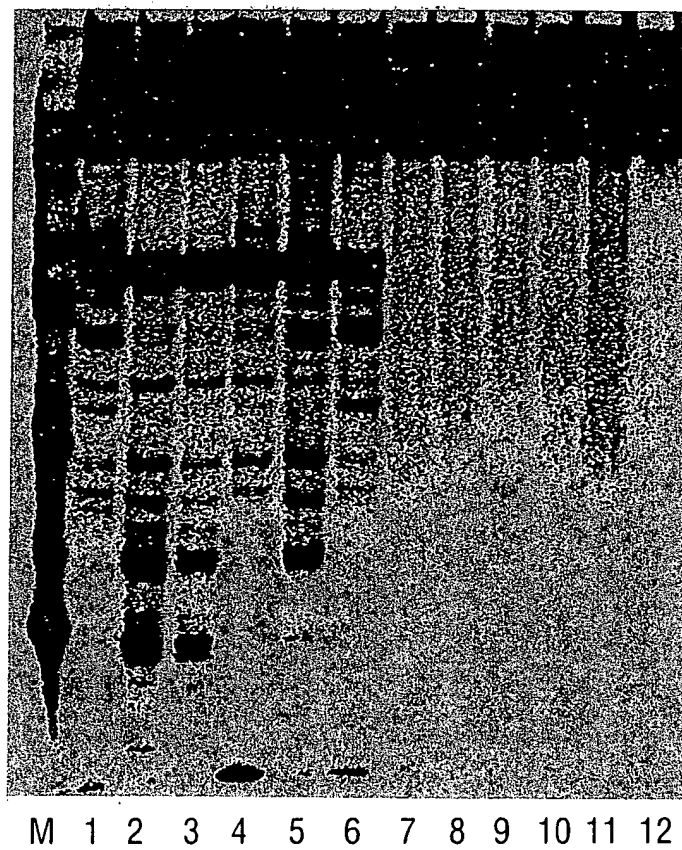


FIG. 50

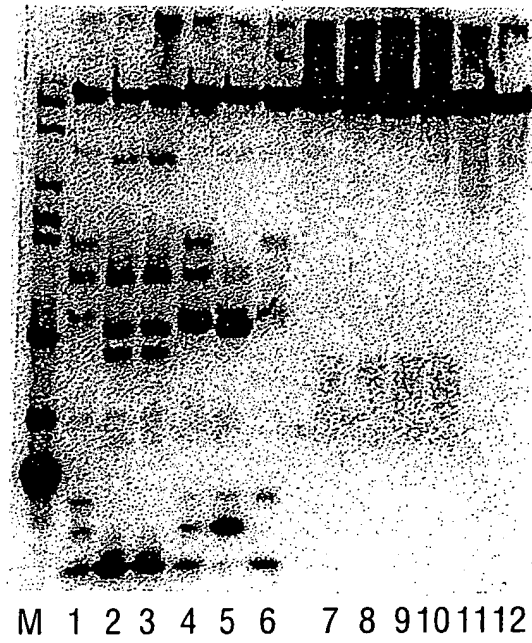


FIG. 51

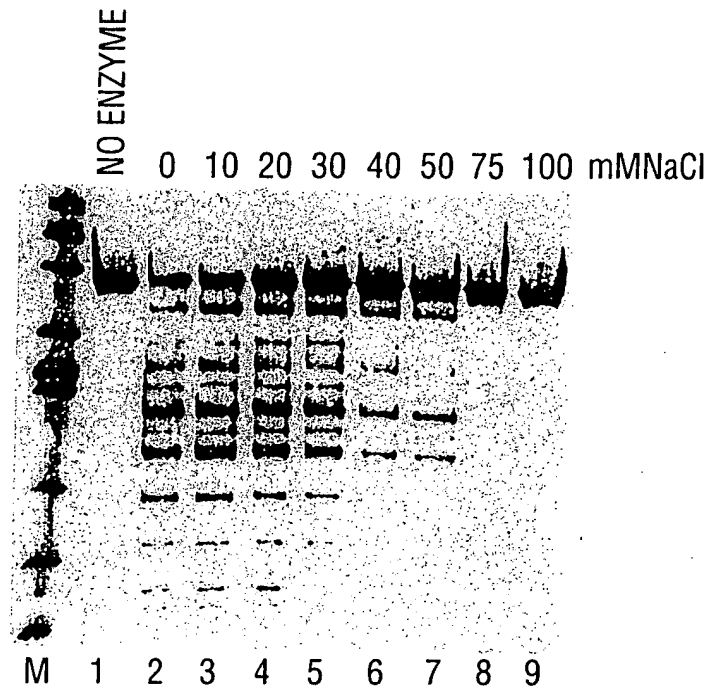


FIG. 52

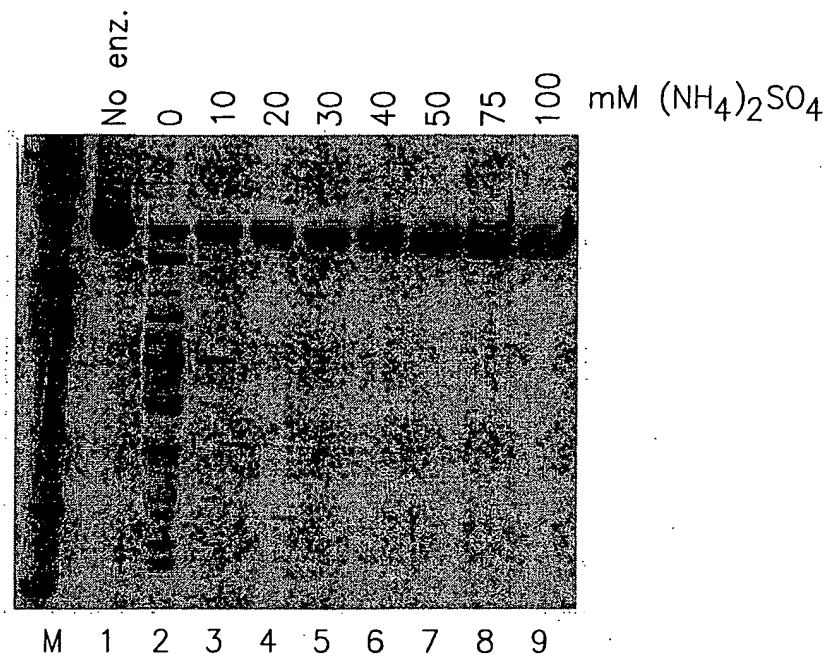


FIG. 53

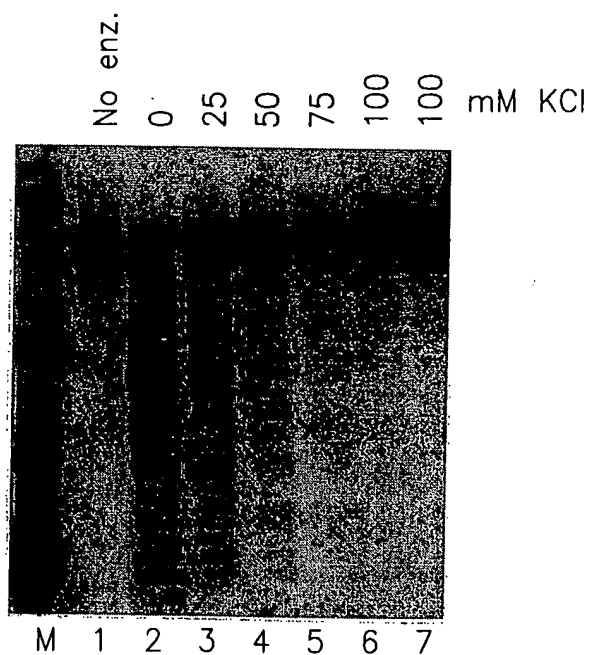


FIG. 54

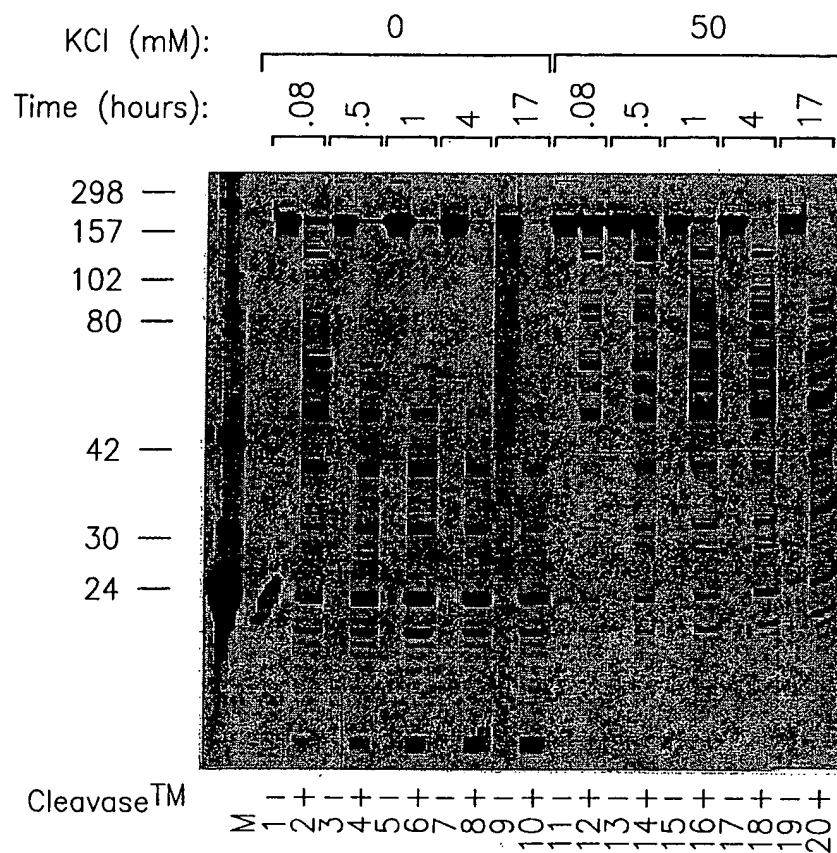


FIG. 55

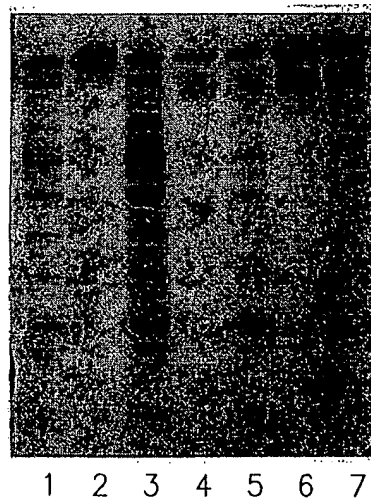


FIG. 56

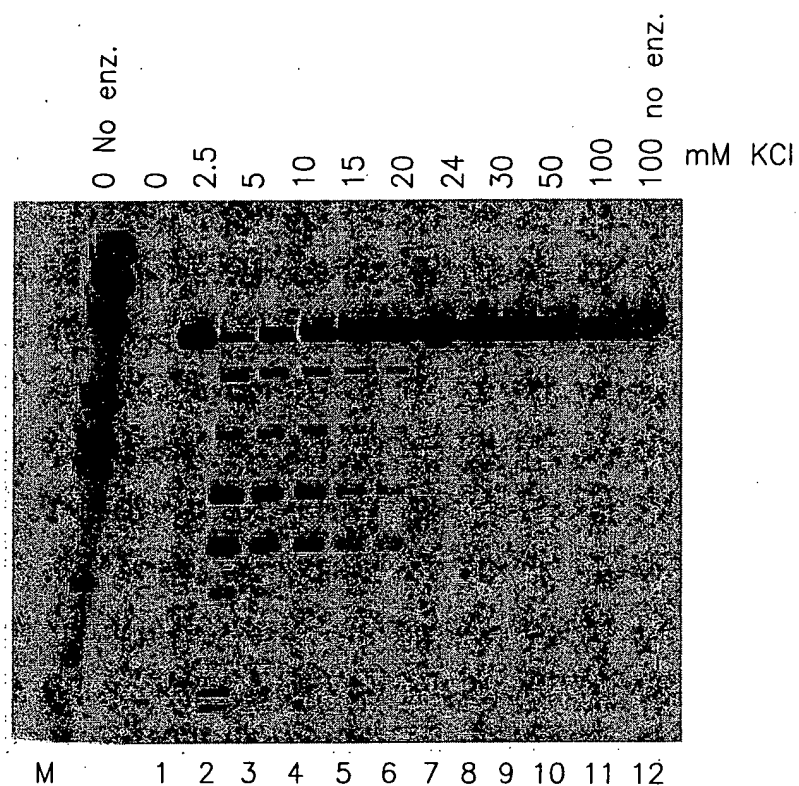


FIG. 57

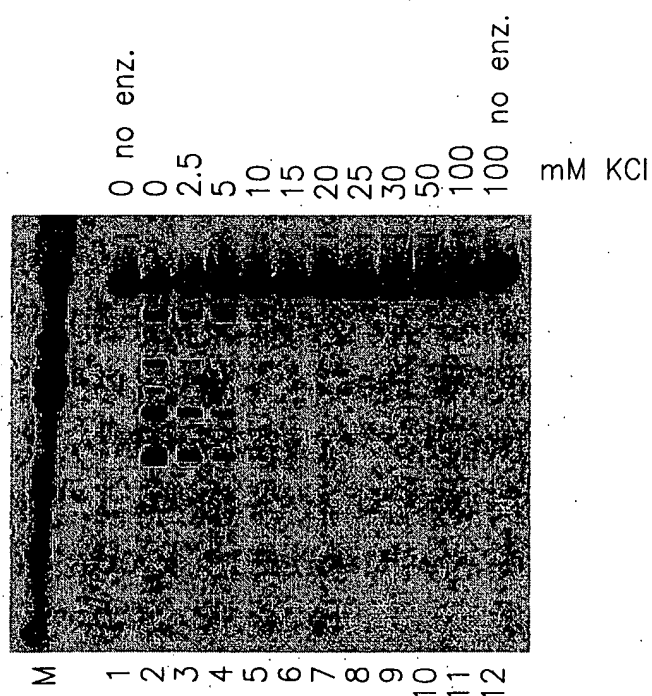


FIG. 58

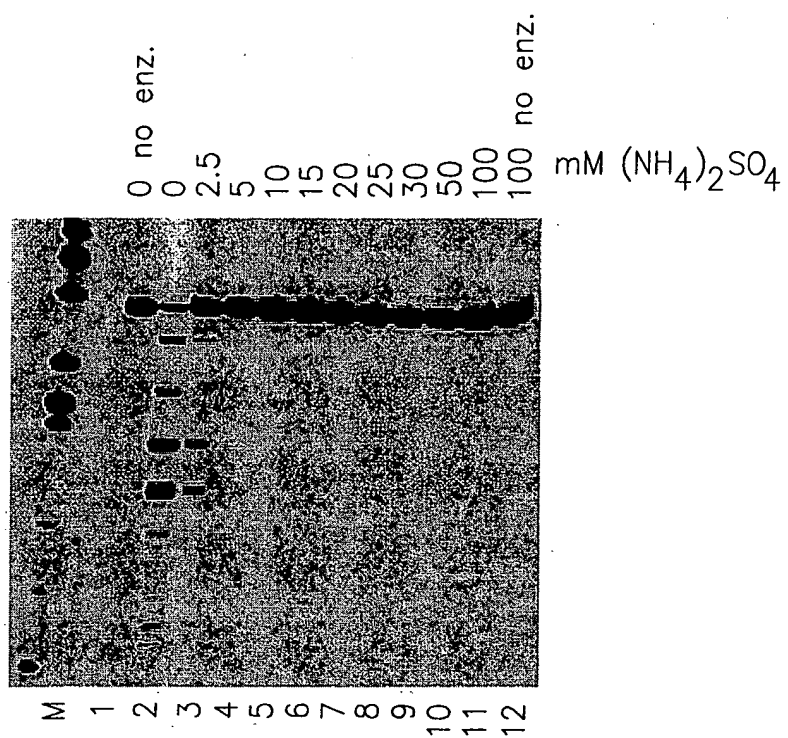


FIG. 59

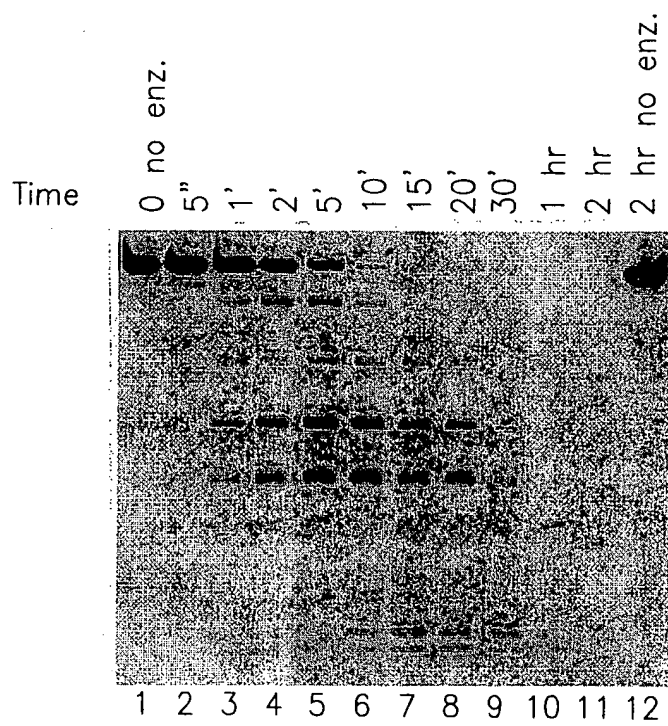


FIG. 60

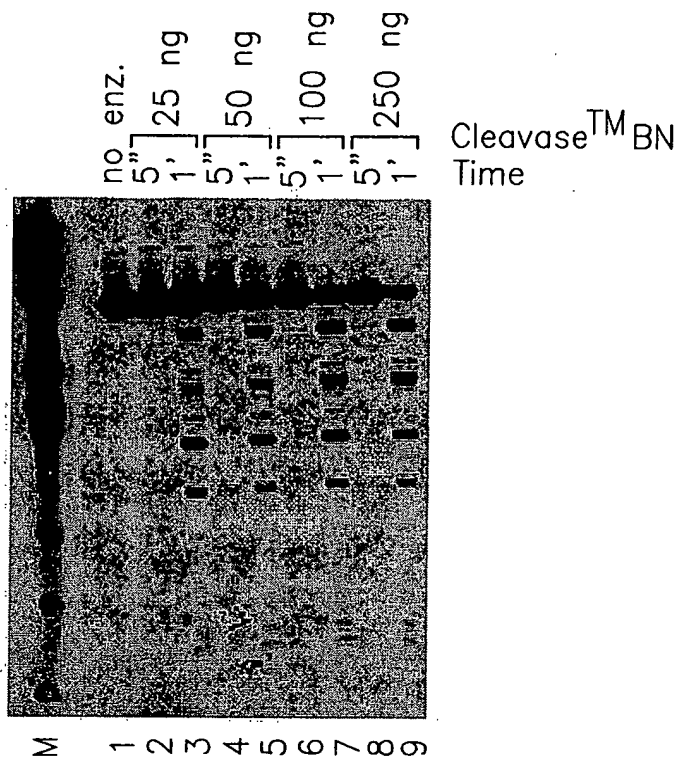


FIG. 61

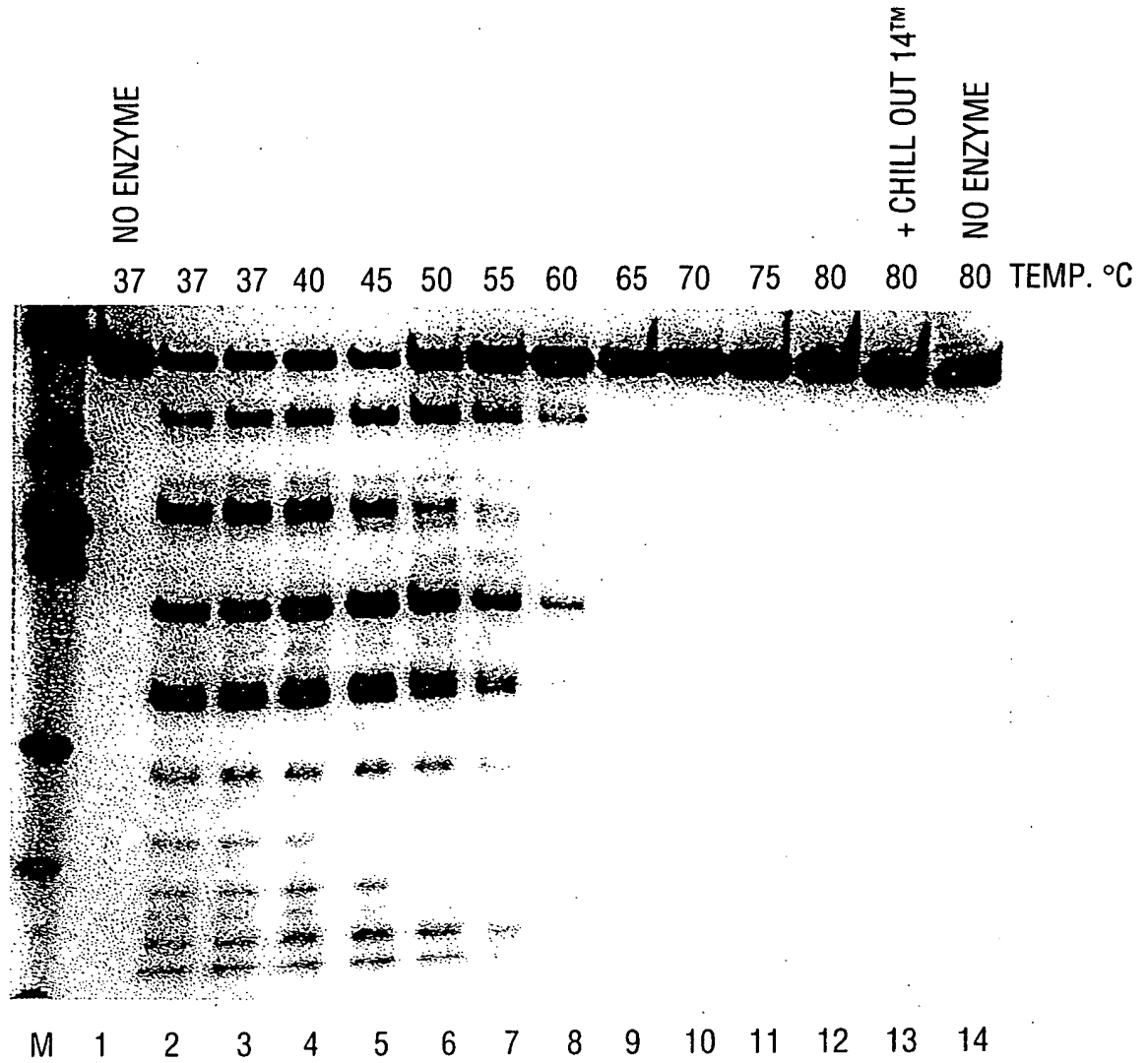


FIG. 62

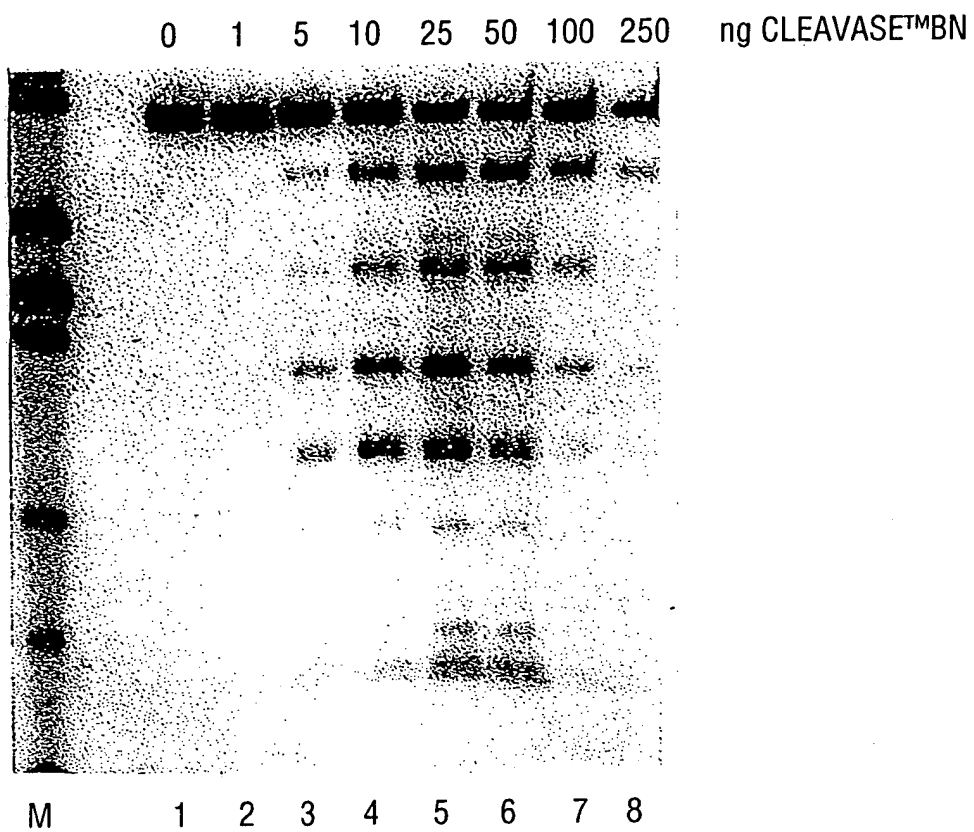
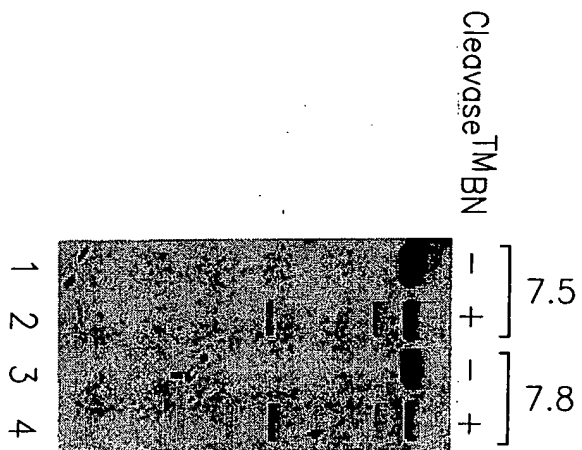
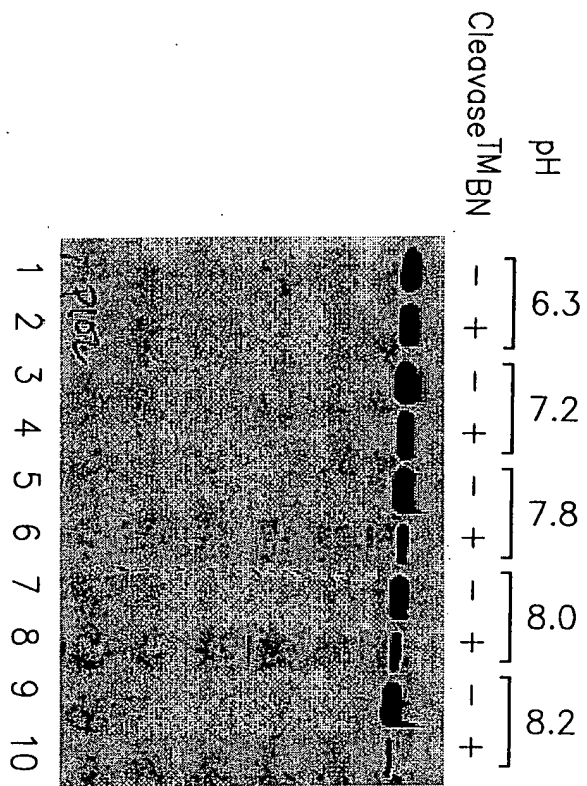


FIG. 63



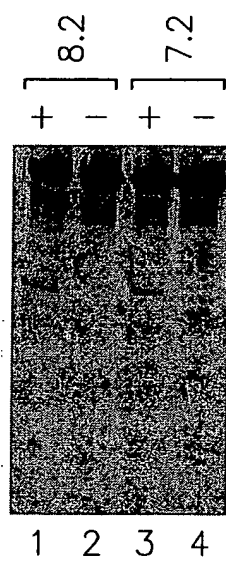


FIG. 65A

pH
CleavaseTMBN

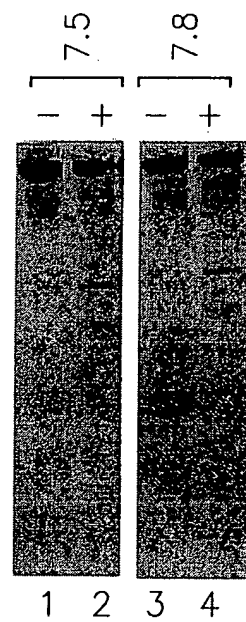


FIG. 65B

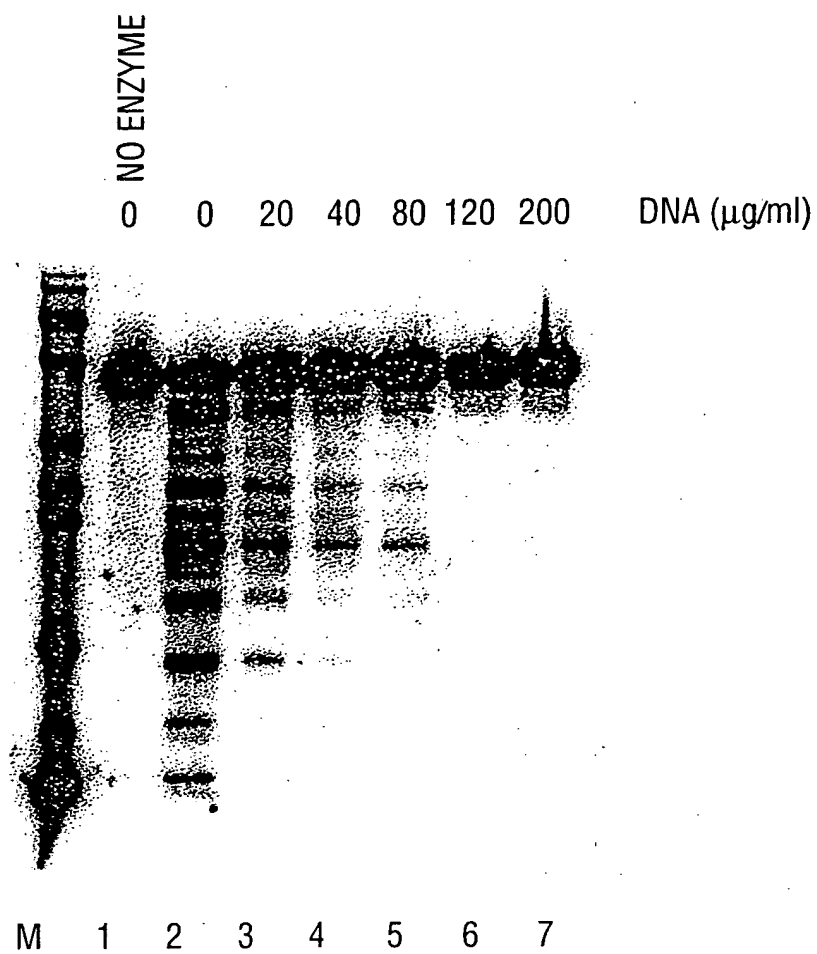


FIG. 66

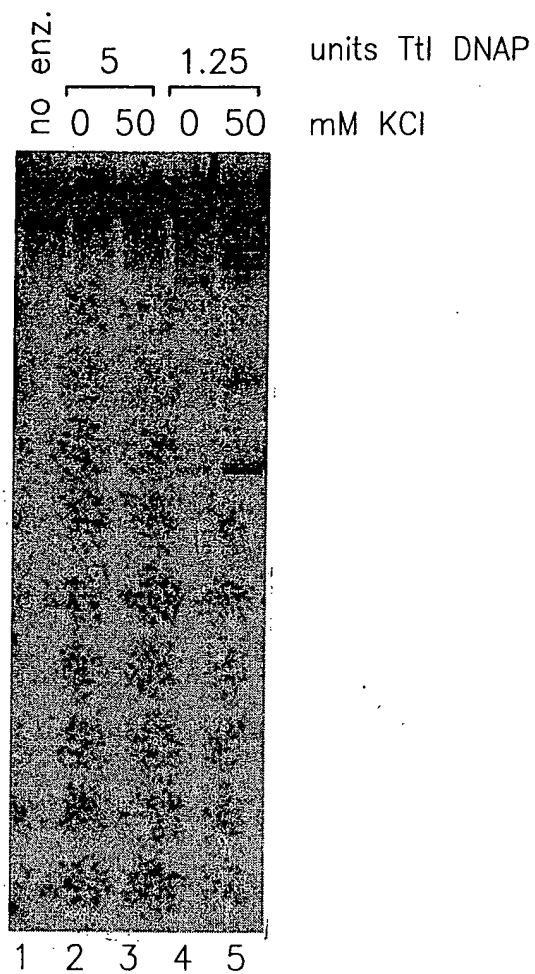


FIG. 67

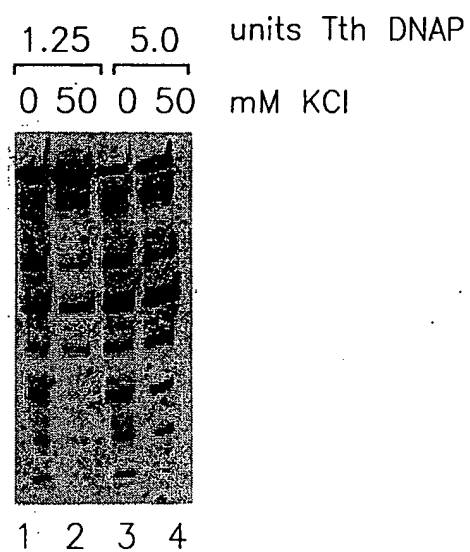


FIG. 68

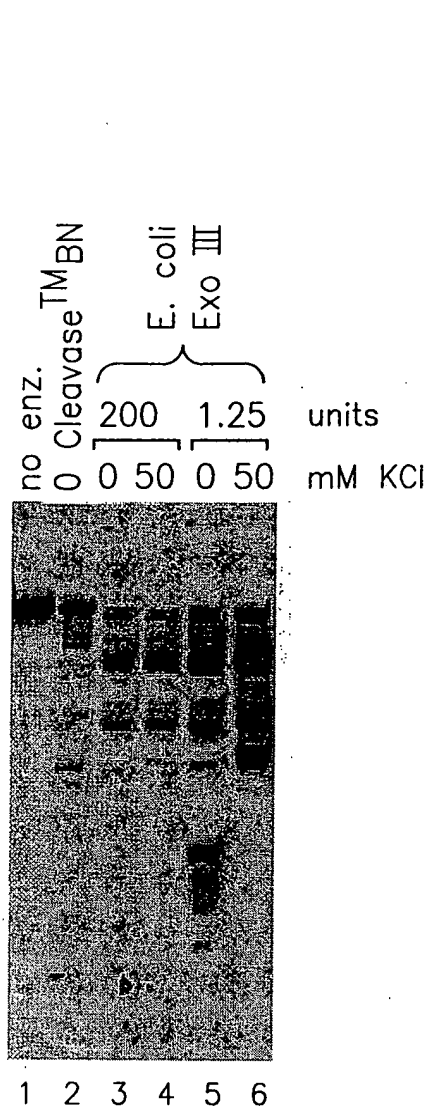


FIG. 69

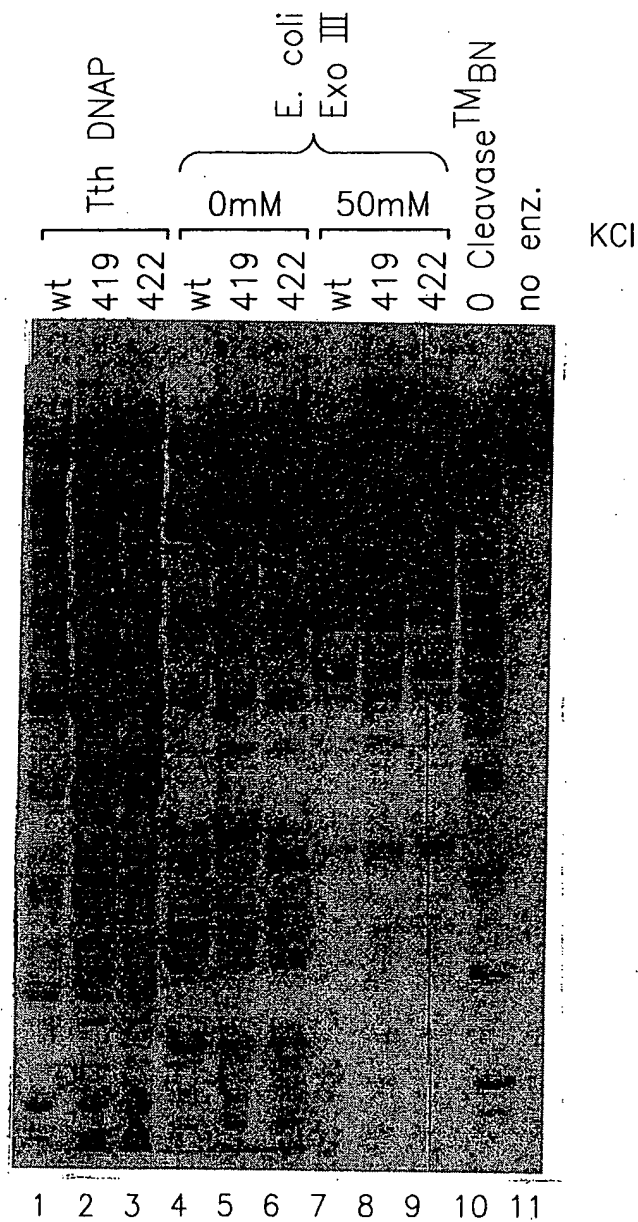
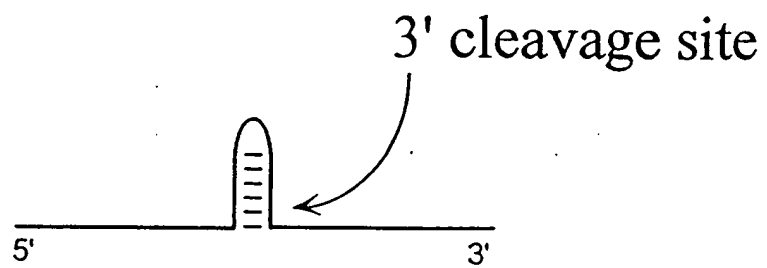
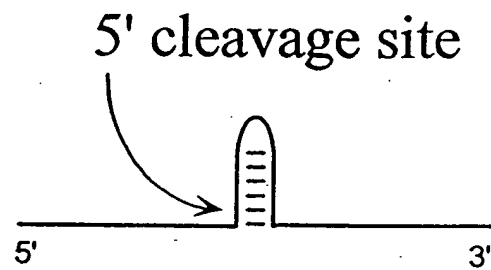
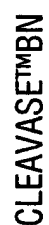


FIG. 70

FIG. 71

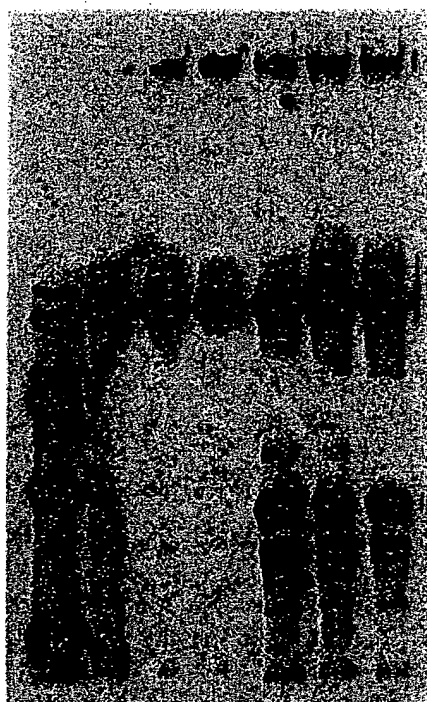




Rad 1/Rad 10

FIG. 72

174



M 1 2 3 4 5 6

FIG. 73

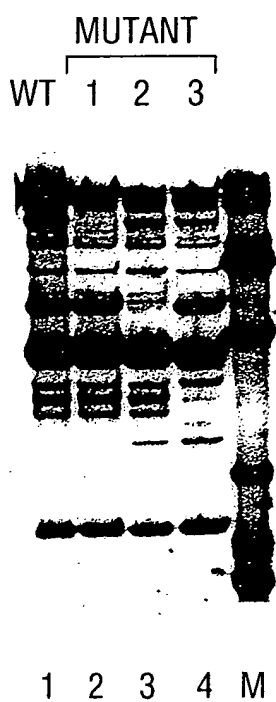


FIG. 74A

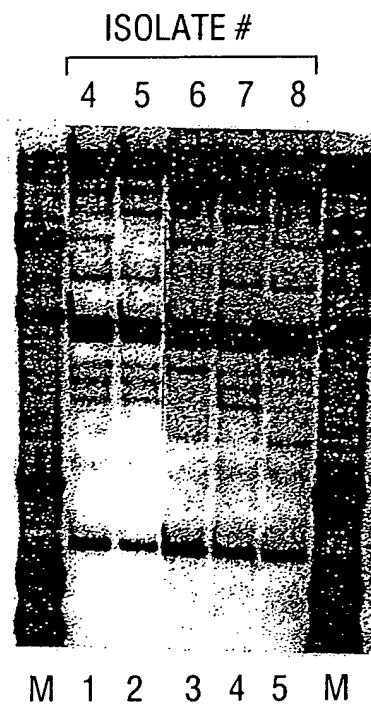


FIG. 74B

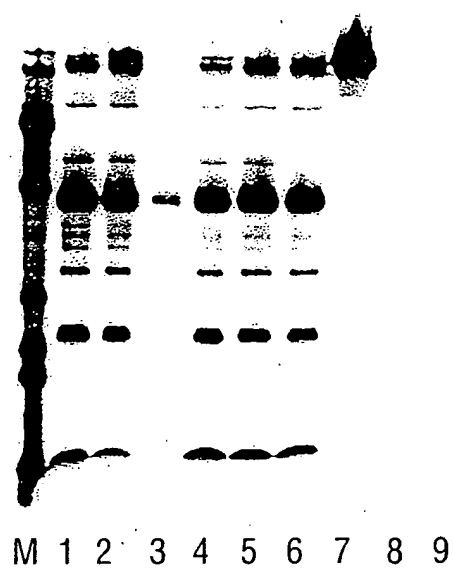


FIG. 75

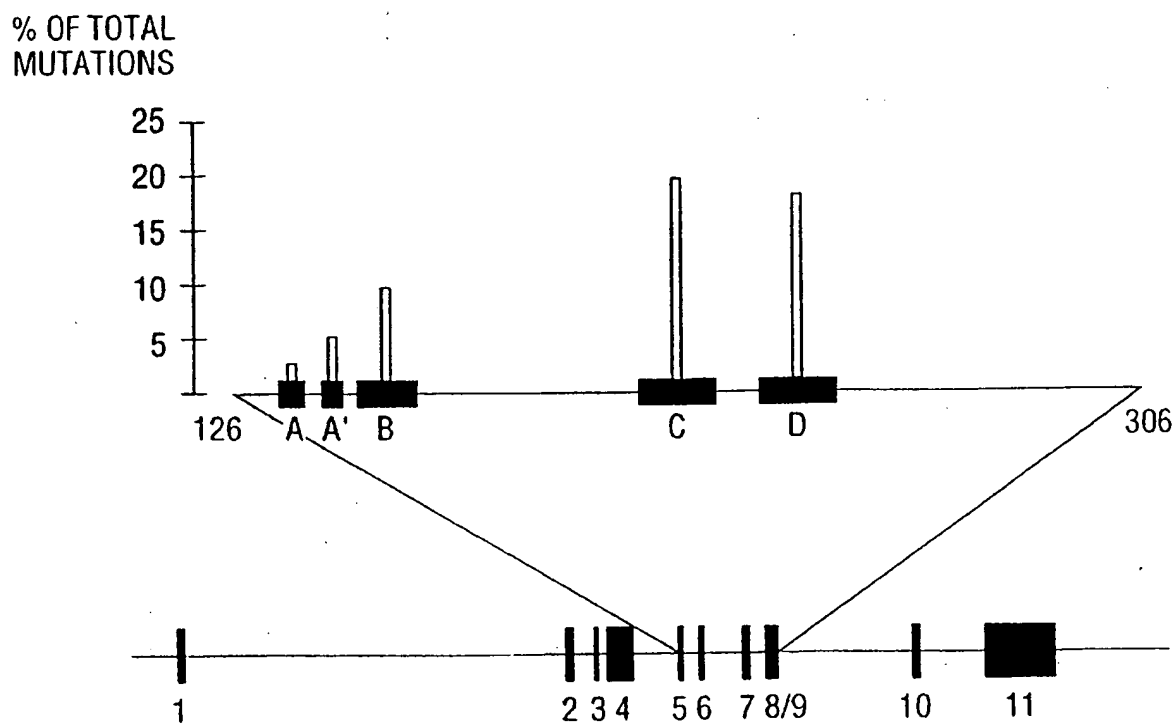


FIG. 76

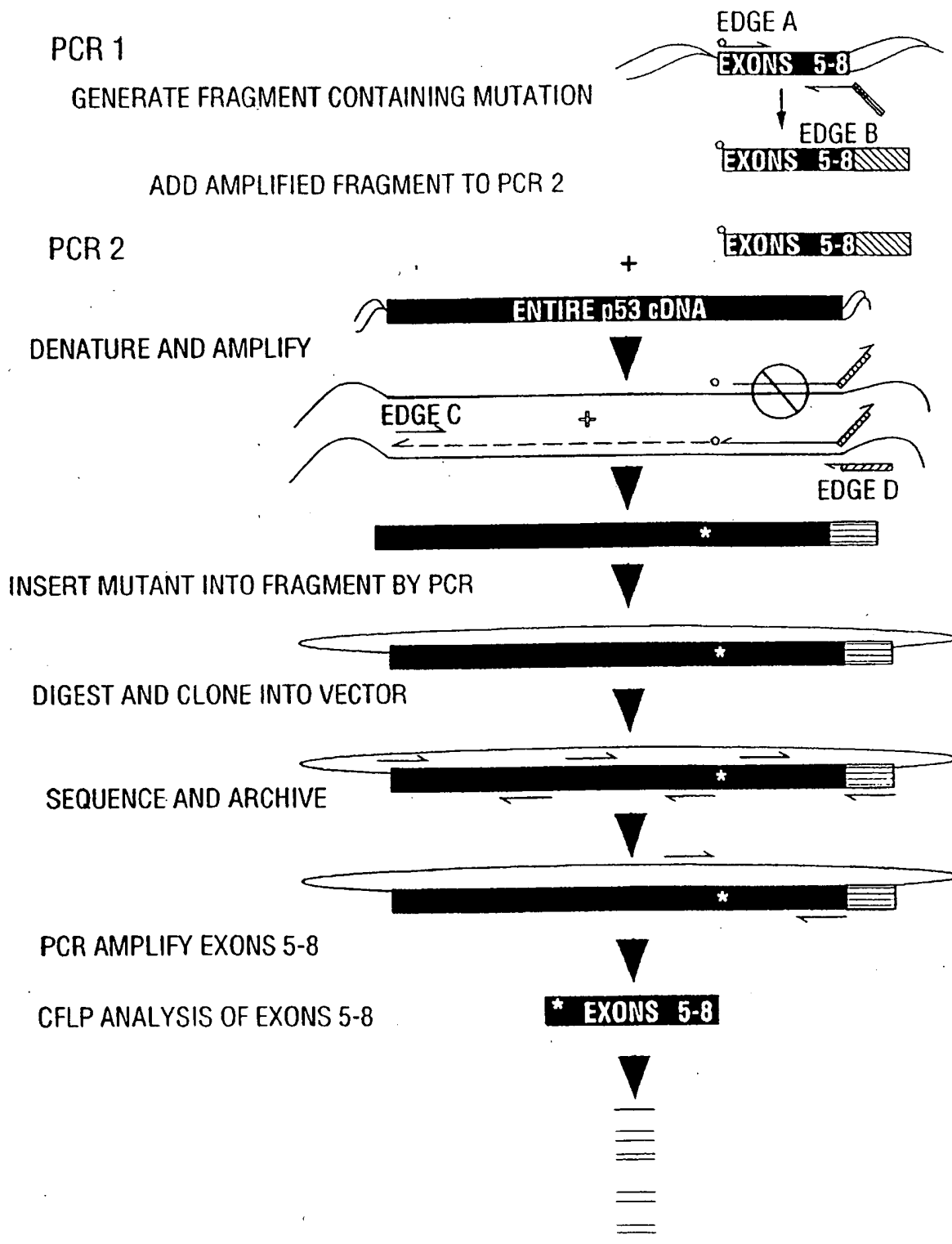


FIG. 77

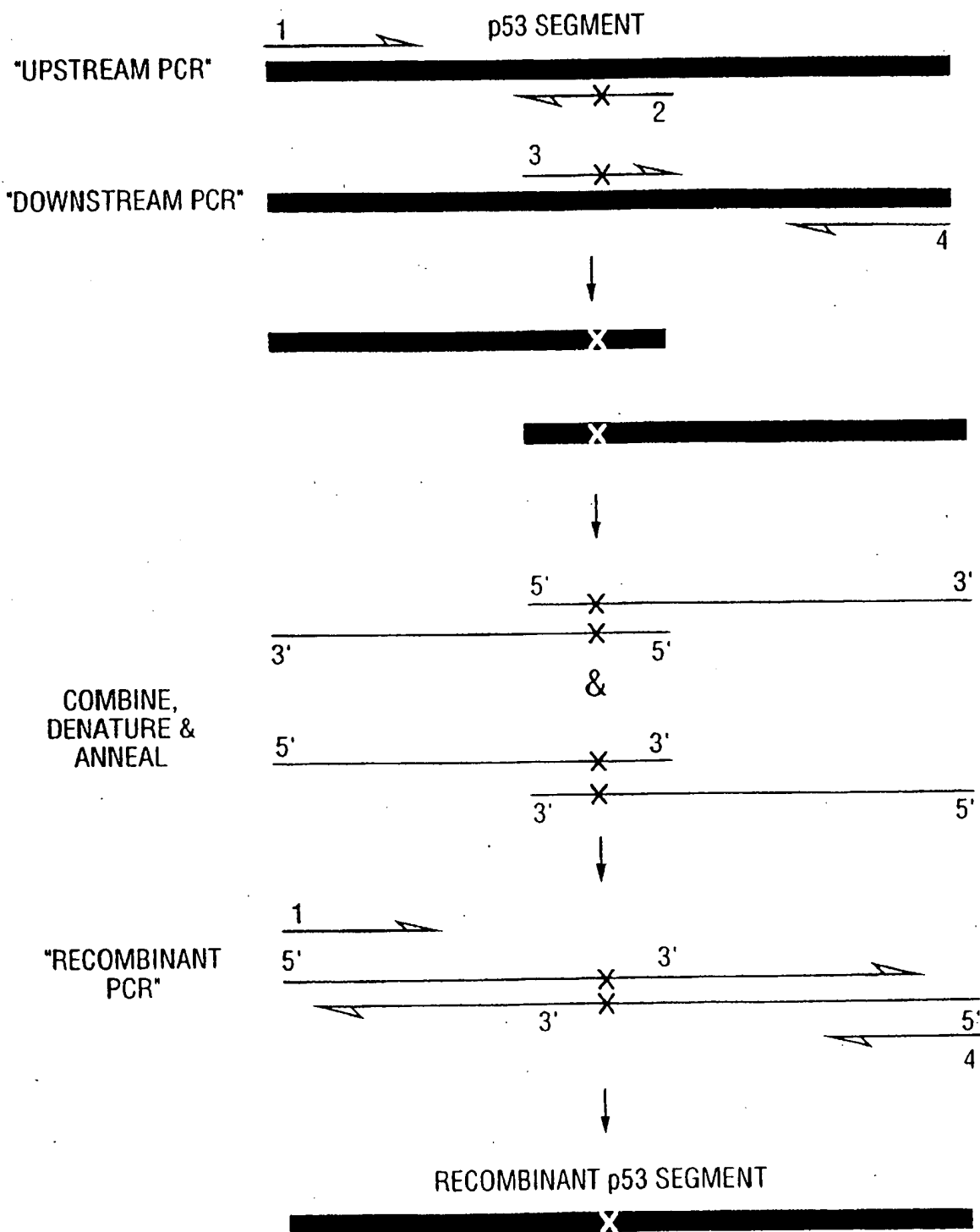


FIG. 78

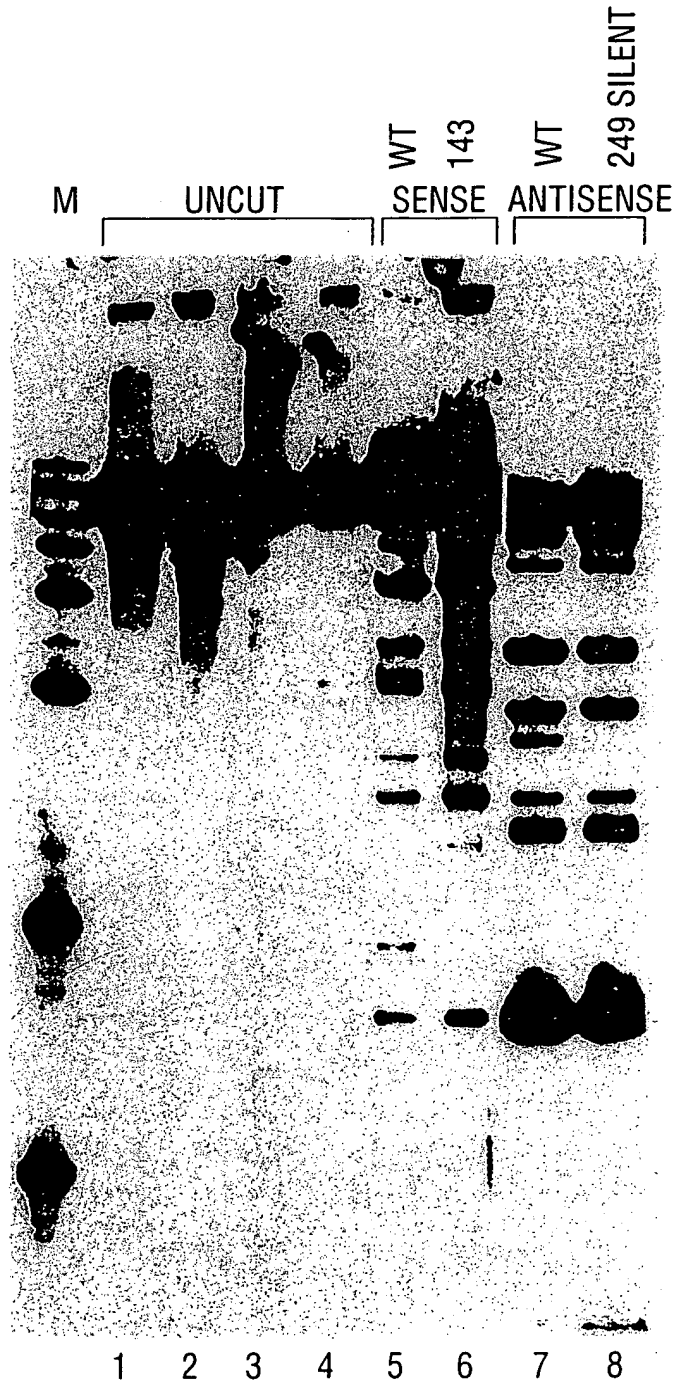


FIG. 79

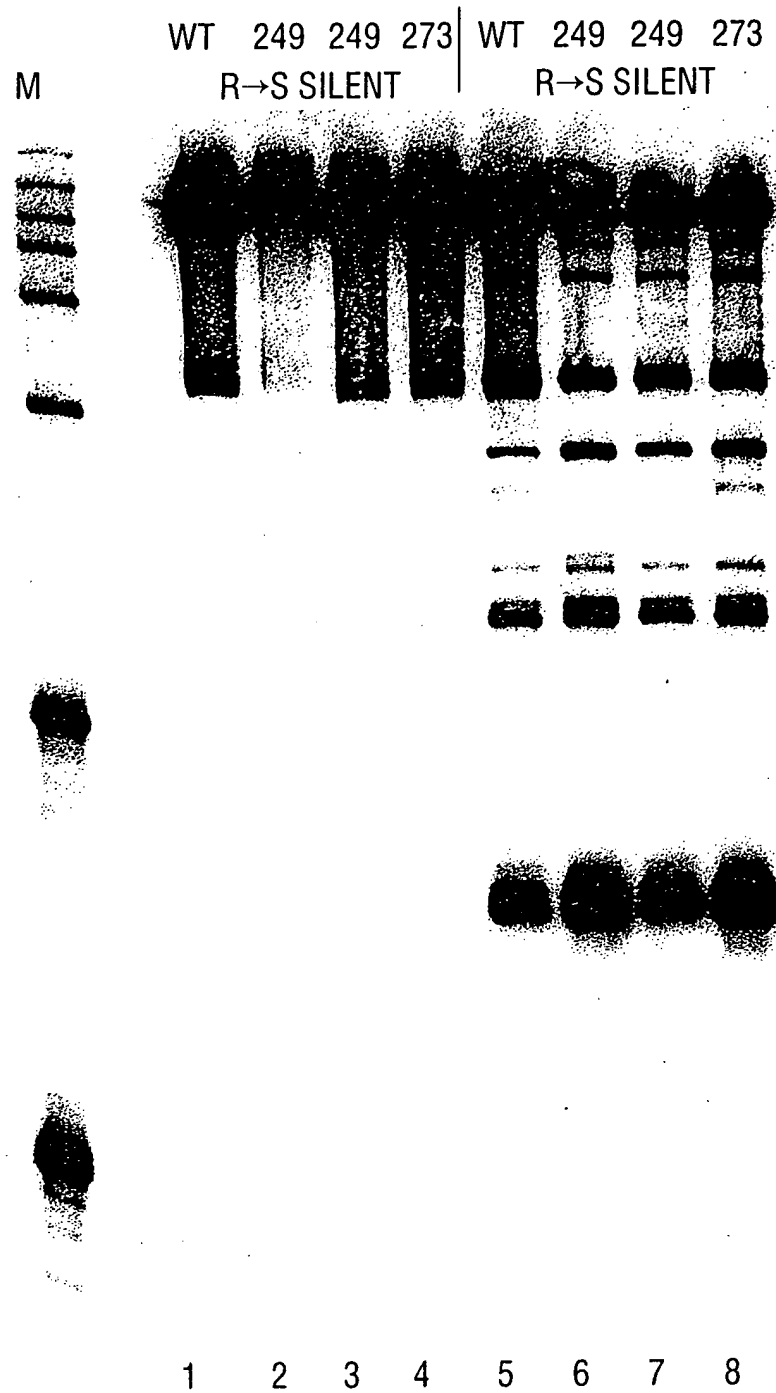


FIG. 80

MIXING PROPORTIONS

M	UNCUT	1	1	1	1	0	2	4	9	WILD TYPE
	WT MUT	0	1	2	9	1	1	1	1	MUTANT

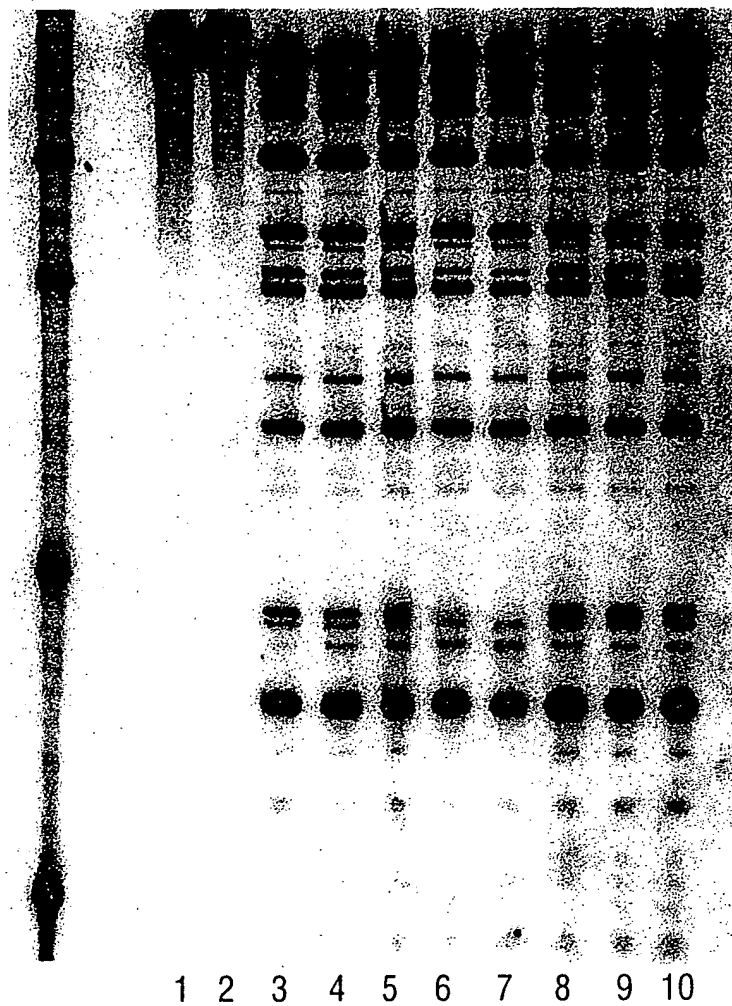


FIG. 81

FIG. 82

HCV1.1	(SEQ ID NO:121)	1	CTGTCTTCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTGCTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV7.1	(SEQ ID NO:126)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTGCTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGT	CTGCCGAACC	
HCV1.1		101	GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT- <u>AAA</u>	150
HCV2.1			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT- <u>CAA</u>	
HCV3.1			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT- <u>CAA</u>	
HCV4.2			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT- <u>CAA</u>	
HCV6.1			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT- <u>CAA</u>	
HCV7.1			GGTAGTACA	CCGGAATTGC	CAGGACGACC	GCGTCCTTC	TTGGAT- <u>CAA</u>	
HCV1.1		151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV4.2			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV1.1		201	AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	250
HCV2.1			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV3.1			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV4.2			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV6.1			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV7.1			AGTAGTGTG	GGTCGCGAAA	GCGCTTGTG	TACTGCTGA	TAGGCTGCTT	
HCV1.1		251	GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV3.1			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV4.2			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV6.1			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV7.1			GCGAGTGCC	CGGAGGTCT	CGTAGACCGT	GC		

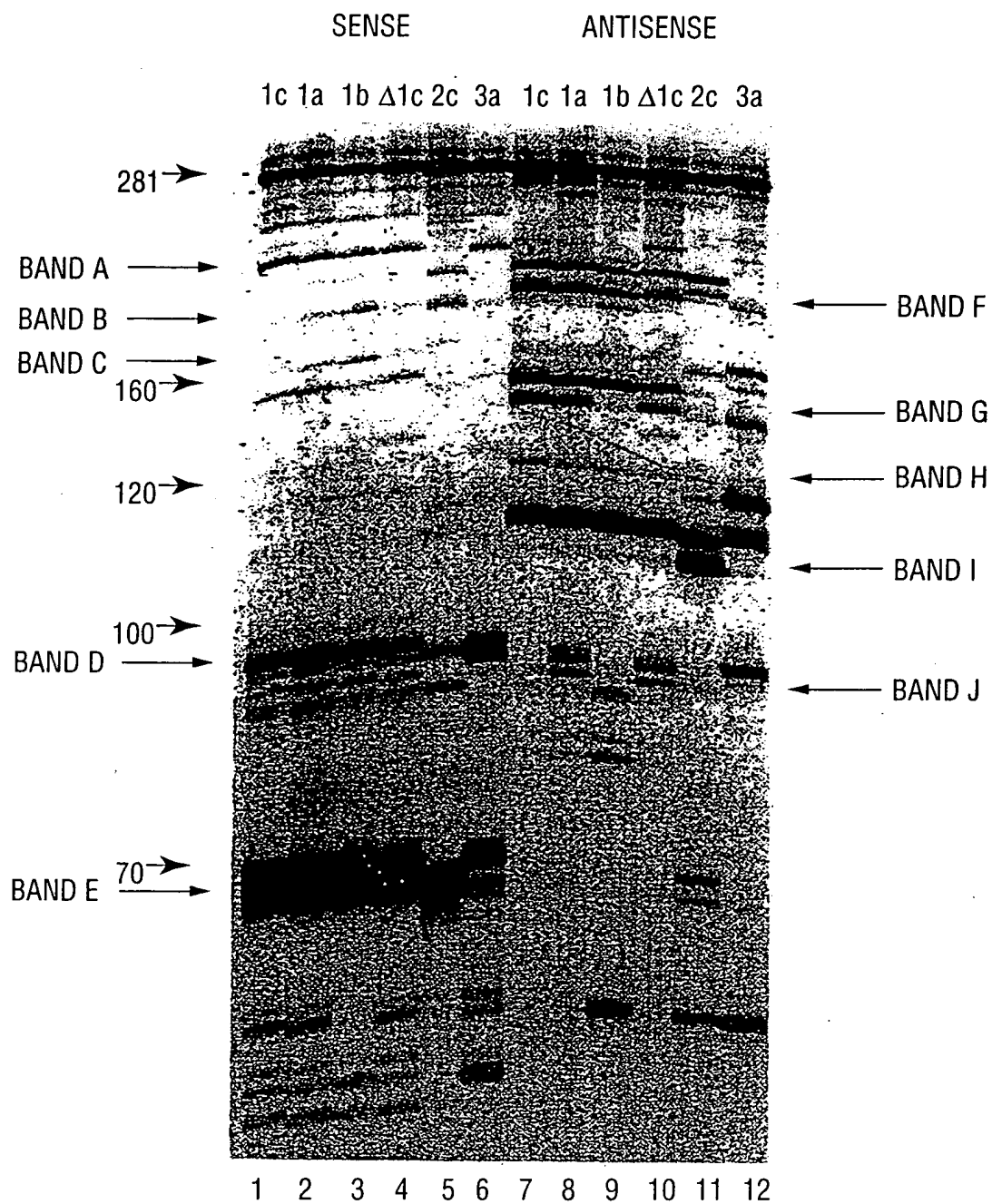


FIG. 83

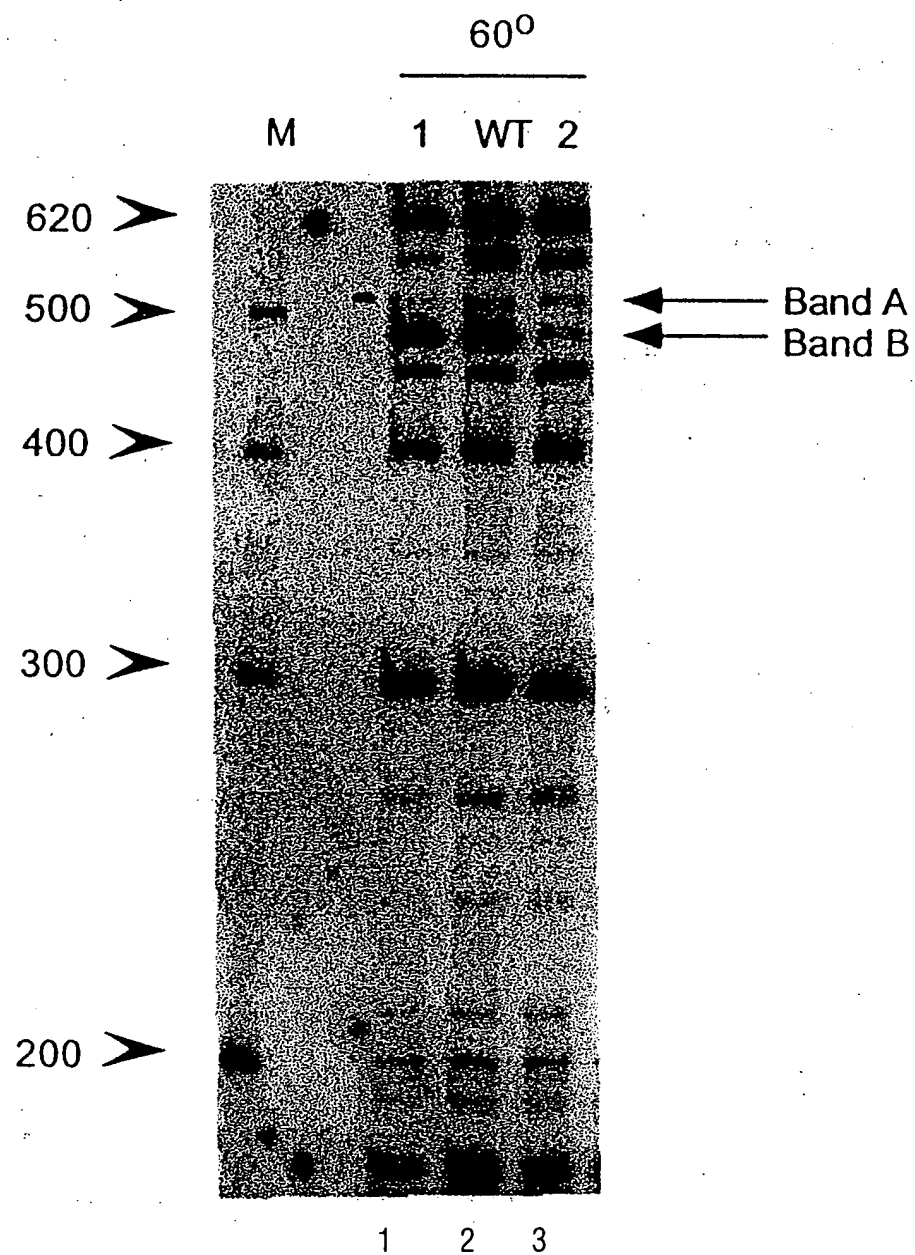


FIG. 84

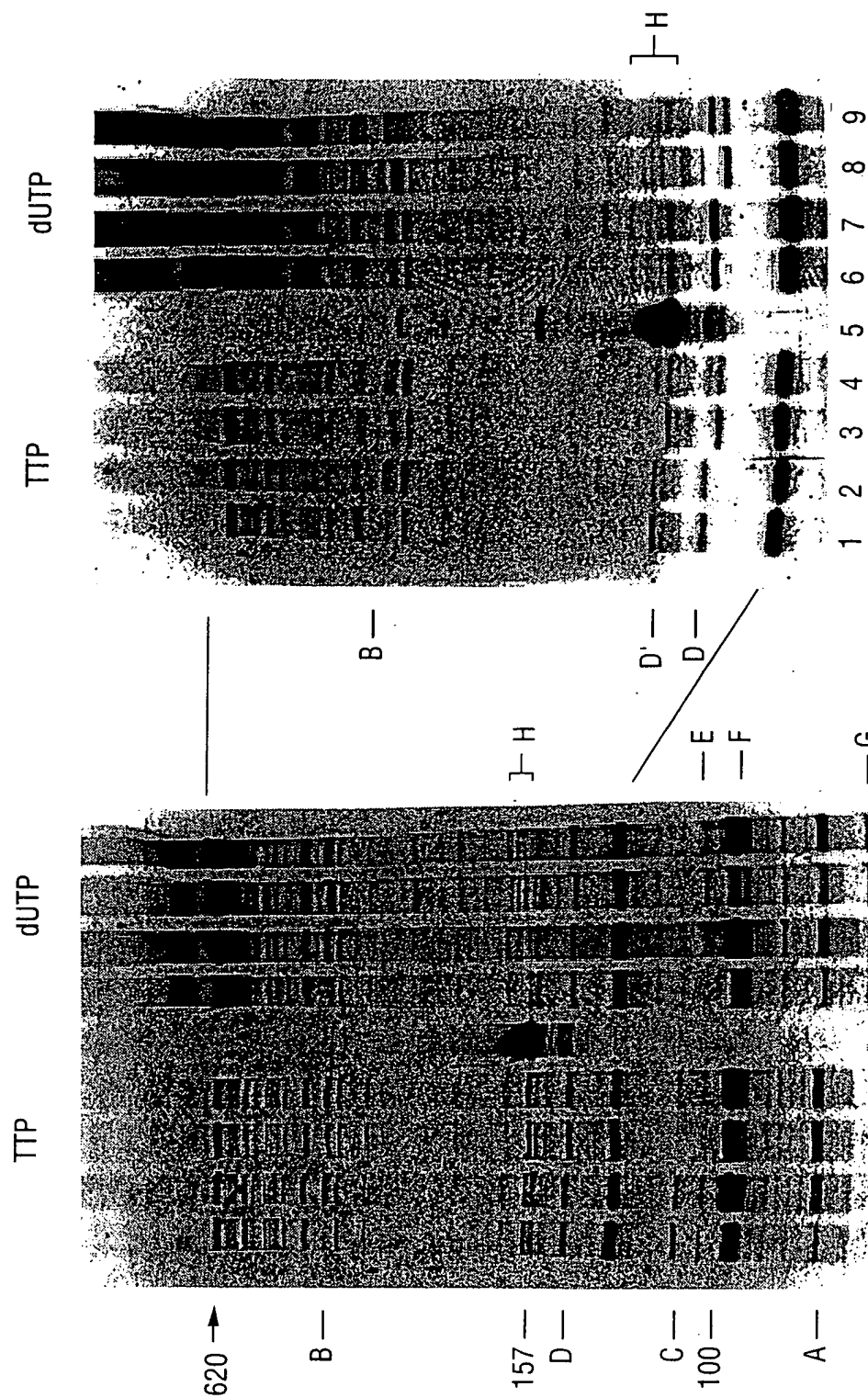


FIG. 85A

FIG. 85B

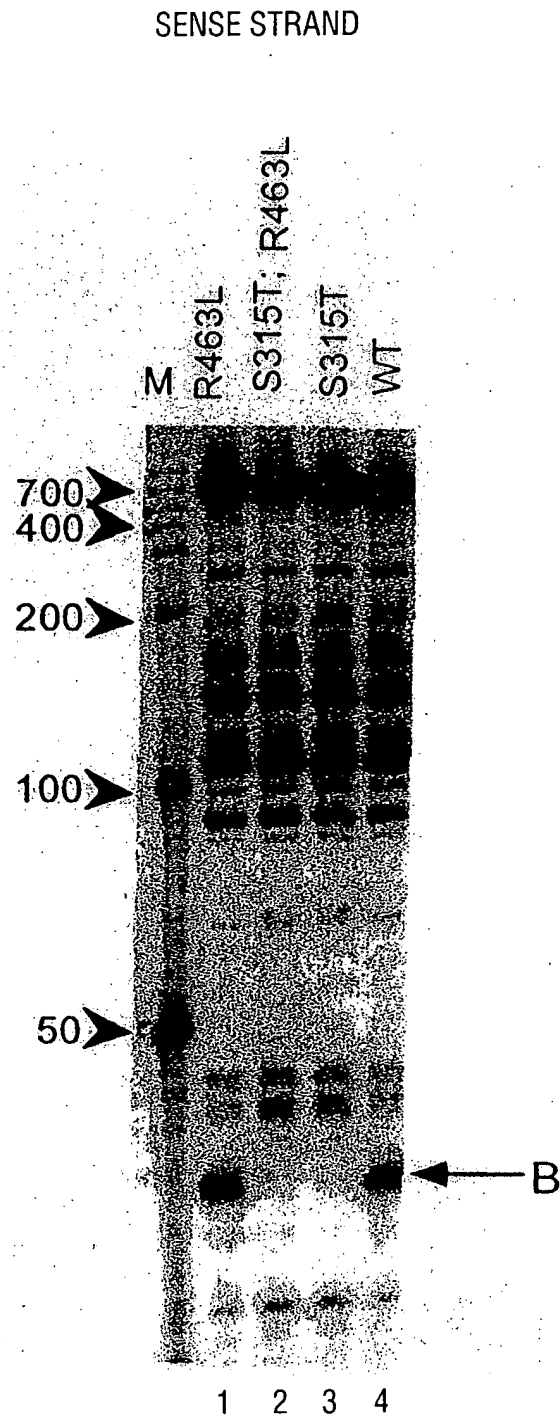


FIG. 86

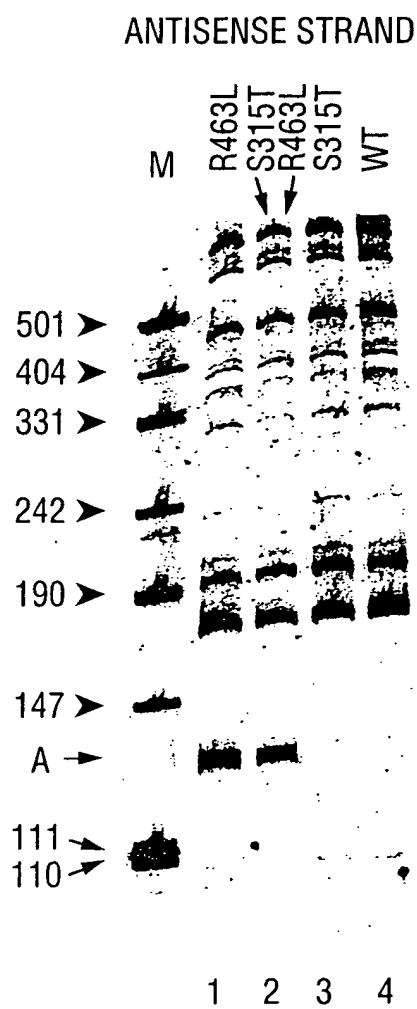


FIG. 87

10	20	30	40	50	60	
AGA GTT	GATCCT	GGCTCAG				
AAATTGA	<u>AGAG</u>	GTTGATCAI	GGCTCAGATT	GAACGCTGGC	GGCAGGCCCTA	ACACATGCAA
TTTA	ACTTCT	CAA	ACTAGTA	CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT
						TGTGTACGTT
70	80	90	100	110	120	
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	AGTGGCGGAC	GGGTGAGTAA	
CAGCTTGCCA	TTGTCCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACCTCAT	
						ER10
130	140	150	160	170	180	
TGCTCTGGGAA	ACTGCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT	
ACAGACCCCTT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA	
190	200	210	220	230	240	
AACGTCGCAA	GACCAAGAGAG	GGGACCTTTC	GGGCTCTTTG	CCATCGGATG	TGCCCAGATG	
TTGCAGCGTT	CTGTTTCTC	CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC	
250	260	270	280	290	300	
GGATTAGCTA	GTAGGTGGGG	TAACGGCTCA	CCTAGGCGAC	GATCCCTAGC	TGGTCTGAGA	
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAAGACTCT	
310	320	330	340	350	360	
GGATGACCCAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGGAG	GCAGCAGTGG	
CCTACTGGTC	GGTGTGACCT	TGACTCTGTG	CCAGGCTGA	GGATGCCCTC	CGTGGTACCC	
						1659
						TGA GGATGCCCTC CGTCGTC

FIG. 88A

370	380	390	400	410	420
GGAATATTGC	ACCAATGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCCT
CCTATAACG	TGTTACCCCG	GTTCCGACTA	CGTCGGTACG	GGCACATAC	TTCCTCCGGA
430	440	450	460	470	480
TCGGGTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCAACAT	TTCATGAAG	TCGCCCCCTC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGCGGTT	TGTTAAGTCA
CCACGTTCCG	AATTAGCCTT	AATGACCCGC	ATTTCGGGTG	CGTCCGCCAA	ACAATTTCAGT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCCGAG	TTGGACCCCT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCC	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACCTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GGGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCC	CACCCCTCGT

FIG. 88B

790	800	810	820	830	840
AACAGGATTA	GATACCCCTGG	TAGTCCACGC	CGTAACCGAT	GTCGACTTGG	AGGTTGTGCC
TTGTCCTAAT	CTATGGGACC	ATCAGGTGCG	GCATTGTGCTA	CAGCTGAACC	TCCAACACGG
850	860	870	880	890	900
CTTGAGGCGT	GGCTTCCGGA	GCTAACGCGT	TAAGTCGACC	GCCTGGGGAG	TACGGCCGCA
GAACTCCGCA	CCGAAGGCTT	CGATTGCGCA	ATTCAGCTGG	CGGACCCCTC	ATGCCGGCGT
910	920	930	940	950	960
AGGTTAAAC	TCAAATGAAT	TGAGGGGGGC	CCGCACAAGC	GGTGAGCAT	GTGGTTAAT
TCCAATTTTG	AGTTACTTA	ACTGCCCCCG	GGCGTGTTCG	CCACCTCGTA	CACCAAAATTA
970	980	990	1000	1010	1020
TCGATGCAAC	GCGAAGAACC	TTACCTGGTC	TTGACATCCA	CGGAAGTTT	CAGAGATGAG
AGCTACGTTG	CGCTTCTTGG	AATGGACCAG	AACTGTAGGT	GCCTTCAAAA	GTCTCTACTC
1030	1040	1050	1060	1070	1080
AATGTGCCTT	CGGGAACCGT	GAGACAGGTG	CTGCATGGCT	GTGTCAGCT	CGTGTGTGA
TTACACGGAA	GCCCCTTGGCA	CTCTGTCCAC	GACGTACCGA	CAGCAGTCGA	GCACACACACT
1090	1100	1110	1120	1130	1140
	GC	AACGAGCGCA	ACCC		
AATGTTGGGT	TAAGTCCCCG	AACGAGCGCA	ACCCCTTATCC	TTGTTGCCA	GGGTCGGGC
TTACAACCCA	ATTCAGGGCG	TGCTCGCGT	TGGGAATAGG	AAACAACGGT	CGCCAGGCCG
1150	1160	1170	1180	1190	1200
				ATG	ACGTCAAGTC
				ATG	ACGTCAAGTC
CGGGAACCTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGATG	ACGTCAGTTC
GCCCTTGAGT	TTCCTCTGAC	GGTCACTAAT	TGACCTCCTT	CCACCCCTAC	TGCAGTTTCA

FIG. 88C

SB-1

SB-3
SB-4

SB-3
SB-4

1210	1220	1230	1240	1250	1260
ATCATGGCCC TTA					
ATCATGGCCC TTACGA					
<u>ATCATGGCCC</u> <u>TTACGACCAG</u>					
TAGTACC6GG AATGCTGGTC	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAGCG	
	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTCGC	
1270	1280	1290	1300	1310	1320
ACCTCGCGAG AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC	
TGGAGCGCTC TCGTTCGCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG	
1330	1340	1350	1360	1370	1380
TCGACTCCAT GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT	
AGCTGAGGTA CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACCTAATGCA</u>	
			GC	CACCTATGCA	

1743

1390	1400	1410	1420	1430	1440
TCCCCGGCCT TGTACACACC	GCCCCGTCACA	CCATGGGAGT	GGGTGCAAA	AGAAAGTAGT	
<u>AGGGCCCGGA</u> <u>ACATGTGTGG</u>	CGGGCAGTGT	GGTACCCCTCA	CCCAACGTTT	TCTTCATCCA	
AGGGCCCGGA ACATG					

1743

1450	1460	1470	1480	1490	1500
AGCTTAACCT TCGGGAAGGC	GCTTACCACCT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA	
TCGAATTGGA AGCCCTCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT	
1510	1520	1530	1540	1550	
CAAGGTAACC GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....		
GTTCCATTGG CATCCCCCTTG	GACGCCCAAC	TAGTGGAGGA	AT.....		

FIG. 88D

```

1638 (SEQ ID NO:151)
E.colirrsE(SEQ ID NO:158) 0 ..AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCCTAACACATGCA
Cam.jejun5(SEQ ID NO:159) 0 ~TTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCCTGCTTAATACATGCA
Stp.aureus(SEQ ID NO:160) 0 ..TTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCCTGCTTAATACATGCA

AGAGTTTGATCCTGGCTCAG
GGCGGACGGG

ER10 (SEQ ID NO:152)
E.colirrsE
Cam.jejun5
Stp.aureus
60 AGTCGAACGGTAACAG-----GAAGAAGCTTGCTTCTTT-----GCTGACGAGTGGCGGACGGG
62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAAAGTGA-----TTAGTGGCGCACGGG
61 AGTCGAGCGAA-----CGGACGAGAAGCTTGCTTCTCTGATG-----TT-AGCGGCGGACGGG

TGAGTAA
ER10
E.colirrsE
Cam.jejun5
Stp.aureus
114 TGAGTAATGTCTGGGA-AACTGCCCTGATGGAGGGGATACTACTGGAACGGTAGCTAATA
114 TGAGTAAGGTATAGTTAATCTGCCCTACACAGAAGGACCAACAGTTGGAAACGACTGCTAATA
113 TGAGTAACACGCTGGATAACCTACCCTATAAGACTGGGATAACTTCGGAAACCGAGCTAATA

E.colirrsE
Cam.jejun5
Stp.aureus
175 CCGCATAC-----GTCGCAAGAC-----CAAAGAGGGGGACCTTCG-GGCCCTTG
176 CTCTATACCTCCTGCTTAACACACAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
175 CCGGATAATATTTTGAACCCGCTGTTCAAAAGTGAAAGACGGT----CTT----GCTGTCA

E.colirrsE
Cam.jejun5
Stp.aureus
221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGTAACGGCTCACCTAGGCGACGA
221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
229 CTTATAGATGATCCGCCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA

E.colirrsE
Cam.jejun5
Stp.aureus
283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACCTGAGACACACGGTCCAGACTCCTA
283 CGCTTAAGCTGGTCTGAGAGGATGATCAGTCACACTGGAACCTGAGACACGGTCCAGACTCCTA
291 TACGTAGCCGACCTGAGAGGGGTGATCGGCCACACTGGAACCTGAGACACGGTCCAGACTCCTA
ACTCCTA
1659(COMPL)

```

FIG. 89A

E.colirrsE	345	CGGGAGGCAGCAGTGGGGAATATTGCACCAATGGGCGGCAAGCCTGATGCAGCCATGCCGGGTG
Cam.jejun5	345	CGGGAGGCAGCAGTAGGGAATATTGCCCAATGGGGGAAACCCCTGACGCAGCAACGCCGGGTG
Stp.aureus	353	CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGCGGAAAGCCTGACGGAGCAACGCCGGGTG
1659(COMPL)		CGGGAGGCAGCAG
E.colirrsE	407	TATGAAGAAAGCCCTTCGGGTTGTAAAGTACTTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
Cam.jejun5	407	GAGGATGACACTTTTCGGAGCGTAACCTCCTTTCTTAGGGAAAG-----AATT
Stp.aureus	415	AGTGATGAAGGCTTCGGATCGTAAAACTCTGTTATTAGGGAAGACATATGTAGTAAC
E.colirrsE	468	ACCTTTGCTCATTGACGTTACCCGCAGAAAGACACCGGCTAACTCCGTGCCAGCAGCCGGC
Cam.jejun5	455	C-----TGACGGTACCCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGGC
Stp.aureus	476	_TGTGCACATCTTGACGGGTACCTAATCAGAAAGCCACGGGCTAACTACGTGCCAGCAGCCGGC

FIG. 89B

E. coli irse	530	GTAATACGGAGGGGTGCCAAGCGTTAATCGGAATTACTGGGGCGTAAAGCCGACCGAGGGCGTTT
Cam. jejuns	506	GTAATACGGAGGGGTGCCAAGCGTTACTCGGAATCACTGGGGCGTAAAGGGCGCGTAGGGGATT
Stp. aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGGCGTAAAGCGCGCGTAGGGCGTTT
E. coli irse	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACCTGCATCTGATACTGGCAAGCTT
Cam. jejuns	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACCTGCTTGGAACCTGATAGTCTA
Stp. aureus	600	TTAAGTCTGATGTGAAAGCCCAACGGCTCAACCGTGGAAGGTCATTGGAAACTGGAAAACTT
E. coli irse	654	GAGTCTCGTAGAGGGGGGTAGAATTCAGGTGTAGCGGTGAAATGCCGTAGAGATCTGGAGGA
Cam. jejuns	630	GAGTGAGGGGAGAGGCAGATGGAATTGGTGGTGTAGGGGTAAAAATCCGTAGATATCACCAAGA
Stp. aureus	662	GAGTGCAAGAGAGGAAAGTGAATTCCATGTGTAGCGGTGAAATGCCGAGAGATATGGAGGA
E. coli irse	716	ATACCGGTGGCGAAGGCGGCCCCCTGGACGAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA
Cam. jejuns	692	ATACCCATTGCGAAGGCGGATCTGCTGGAACCTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp. aureus	724	ACACCAGTGGCGAAGGCGACTTCTGTGCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGA
E. coli irse	778	GCAAAACAGGATTAGATACCCCTGGTAGTCCACGCGCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam. jejuns	754	GCAAAACAGGATTAGATACCCCTGGTAGTCCACGCGCGTAAACGATGTACACTAGTTGTTGGGT
Stp. aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCGCGTAAACGATGAGTGCTAAGTGTTAGGGG

FIG. 89C

E.colirrfE	840	C-CTTGA-GCCGTGGCTTCCGGAGCTAACCGCGTTAAGTCGACCGCCCTGGGGAGTACGGCCG
Cam.jejun5	816	G-CTAGT-CATCTCAGTAATGACGCTAACGCAATTAAGTGTACCGCCCTGGGGAGTACGGTCC
Stp.aureus	848	GT-TTCCGCCCCCTTAGTGCTGCAGCTAACGCAATTAAGCACTCCGCCCTGGGGAGTACGACCGC
E.colirrfE	900	AAGGTTAAAACTCAAATGAATTGACGGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTAATT
Cam.jejun5	876	AAGATTAAAACTCAAAGGAATAGACGGGGGACCCCGCACAAAGCGGTGGAGCATGTGGTTAATT
Stp.aureus	909	AAGGTTGAAACTCAAAGGAATTGACGGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTAATT
E.colirrfE	962	CGATGCCAACGCGGAAGAACCCTTACCCTGGTCTTGACATCCACGGAAGTTTTCAGAGATGAGAAT
Cam.jejun5	938	CGAAGATACGCGGAAGAACCCTTACCCTGGGCTTGATATCCTAAGAACCCTTTCAGAGATAAGAGG
Stp.aureus	971	CGAAGCAACGCGGAAGAACCCTTACCCTTGACATCCTTTGACAACTCTAGAGATAGAGCC
E.colirrfE	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTGTCAGCTCGTGTGTGA
Cam.jejun5	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTGTCAGCTCGTGTGTGA
Stp.aureus	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGCTGCATGGTGTGTCAGCTCGTGTGA
SB-1		GCAACGAGCGCAACCC
E.colirrfE	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
Cam.jejun5	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTAATTAAGTTGCTAACGGTTCGG-CC
Stp.aureus	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D

SB-3 (SEQ ID NO:157)		ATGACGTCAGTCAATC
SB-4 (SEQ ID NO:154)		ATGACGTCAGTCAATC
E.coli rrse	1142	GGGAACCTCAAAGGAGACTGCCAGTGATAACTGGAGGAAGGTGGGGATGACGTCAGTCAATC
Cam. jejuns	1122	GAGCACTCTAATAGACTGCCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAGTCAATC
Stp. aureus	1152	GGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAGTCAATCATC
SB-3		ATGCCCCCTTA
SB-4		ATGCCCCCTTACGA
E.coli rrse	1204	ATGCCCCCTTACGACCAGGGCTACACACCGTGCTACAATGGCGCATACAAAGAGAGCGACCTC
Cam. jejuns	1183	ATGCCCCCTTATGCCAGGGCGACACACGCTGCTACAATGGCATATAGAAATGAGACGCAATACC
Stp. aureus	1214	ATGCCCCCTTATGATTGGGCTACACACGCTGCTACAATGGACCAATACAAAGGGCAGCGAAACC
E.coli rrse	1266	GCGAGAGCAAGCGGACCTCATAAAGTGCGTCTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam. jejuns	1245	GCGAGGTGGAG-CAAATCTATAAAATATGTCCAGTTCGGATTGTCTCTGCAACTCGAGAG
Stp. aureus	1276	GCGAGGTCAAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.coli rrse	1328	CATGAAGTCGGAATCGCTAGTAATCGTGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam. jejuns	1306	CATGAAGCCGGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp. aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743 (compl)		CGGTGAATACGTTCCCGGGC

FIG. 89E

E. coli irsE	1389	CTGTACACACCCCGCCGTCACACCATGGGAGTGGGTTGCCAAAAGAAGTAGGCTTAACCT
Cam. jejuni	1368	CTGTACTCACC CGCCCGTCACACCATGGAGTTGATTTCACCTGGAAGCCGGAATACT--A-A
Stp. aureus	1399	ATTGTACACACCGCCCGTCACACACGAGAGTTTGTAAACACCCGAAGCCGGTGAGTAACCT
1743 (compl)		CTGTAC
E. coli irsE	1451	TCG- <u>GGAGGGCGCTT</u> ACCATTGTGATTCACTGACTGGGGTGAAGTCGTAACAAGGTAACCG
Cam. jejuni	1427	AC-- <u>T-AGTT</u> ACCCTCCACAGTGGAAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCG
Stp. aureus	1461	TTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAACCG
E. coli irsE	1512	TAGGGGAACCTGCGGTTGGATCACCTCCTTA---
Cam. jejuni	1485	TAGGAGAACCCTGCGGTTGGATCACCTCCT----
Stp. aureus	1523	TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-

FIG. 89F

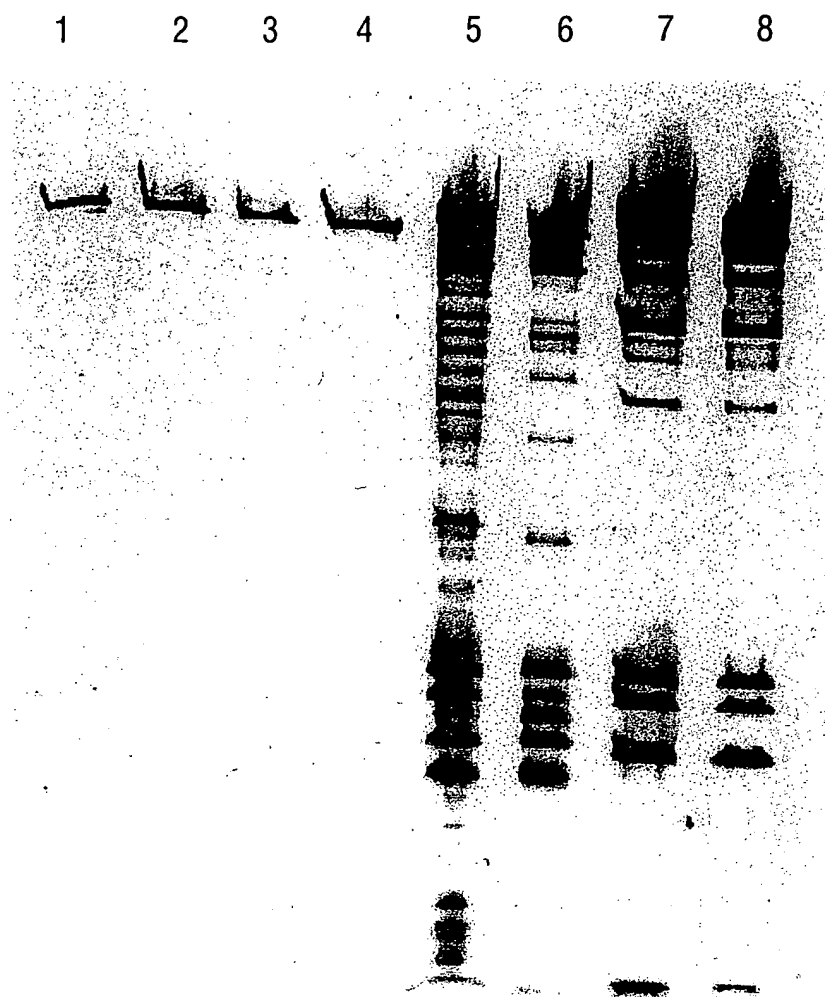


FIG. 90

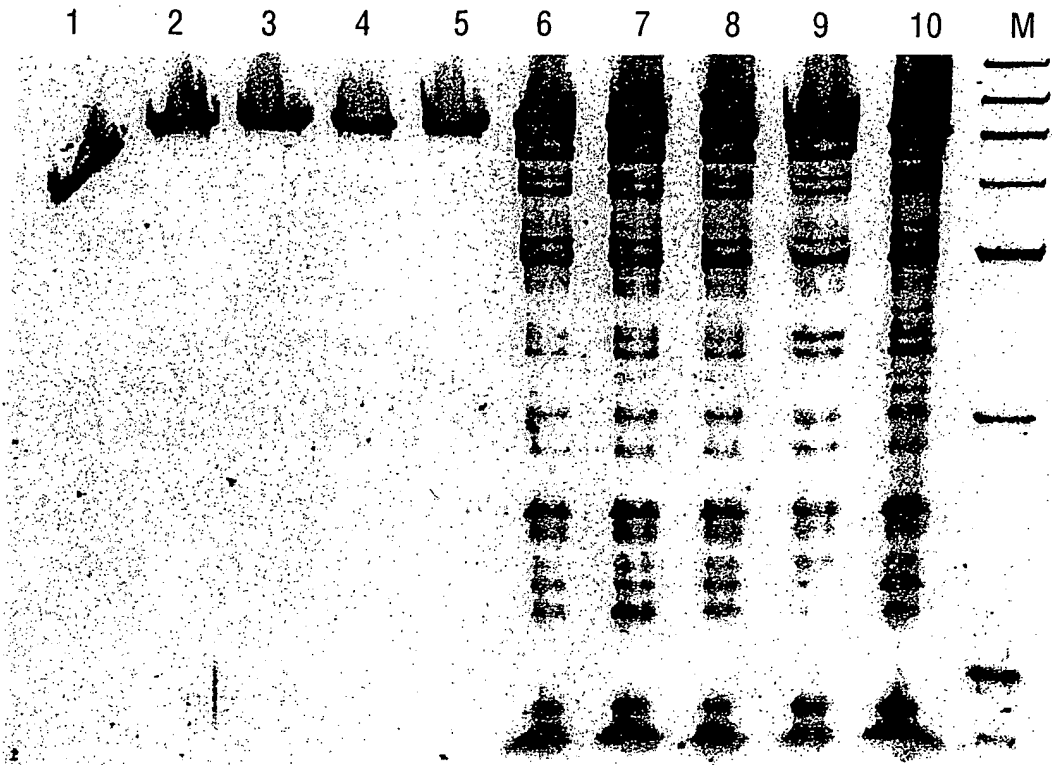


FIG. 91A

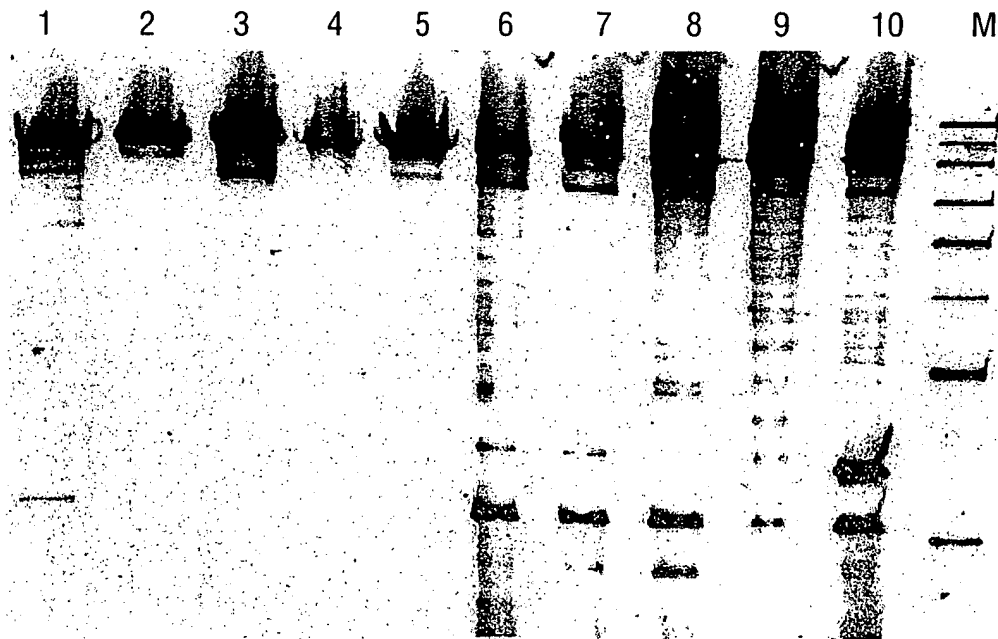


FIG. 91B

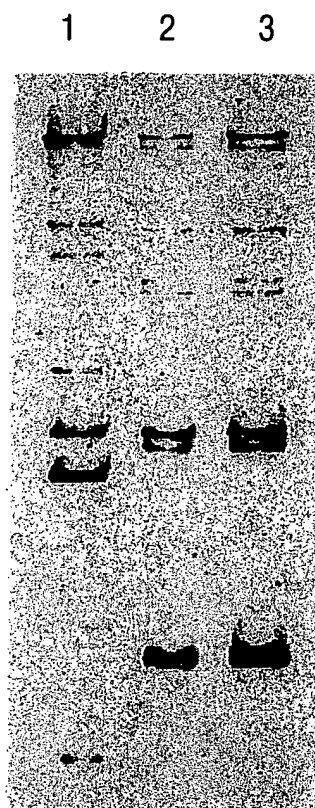


FIG. 92



FIG. 93

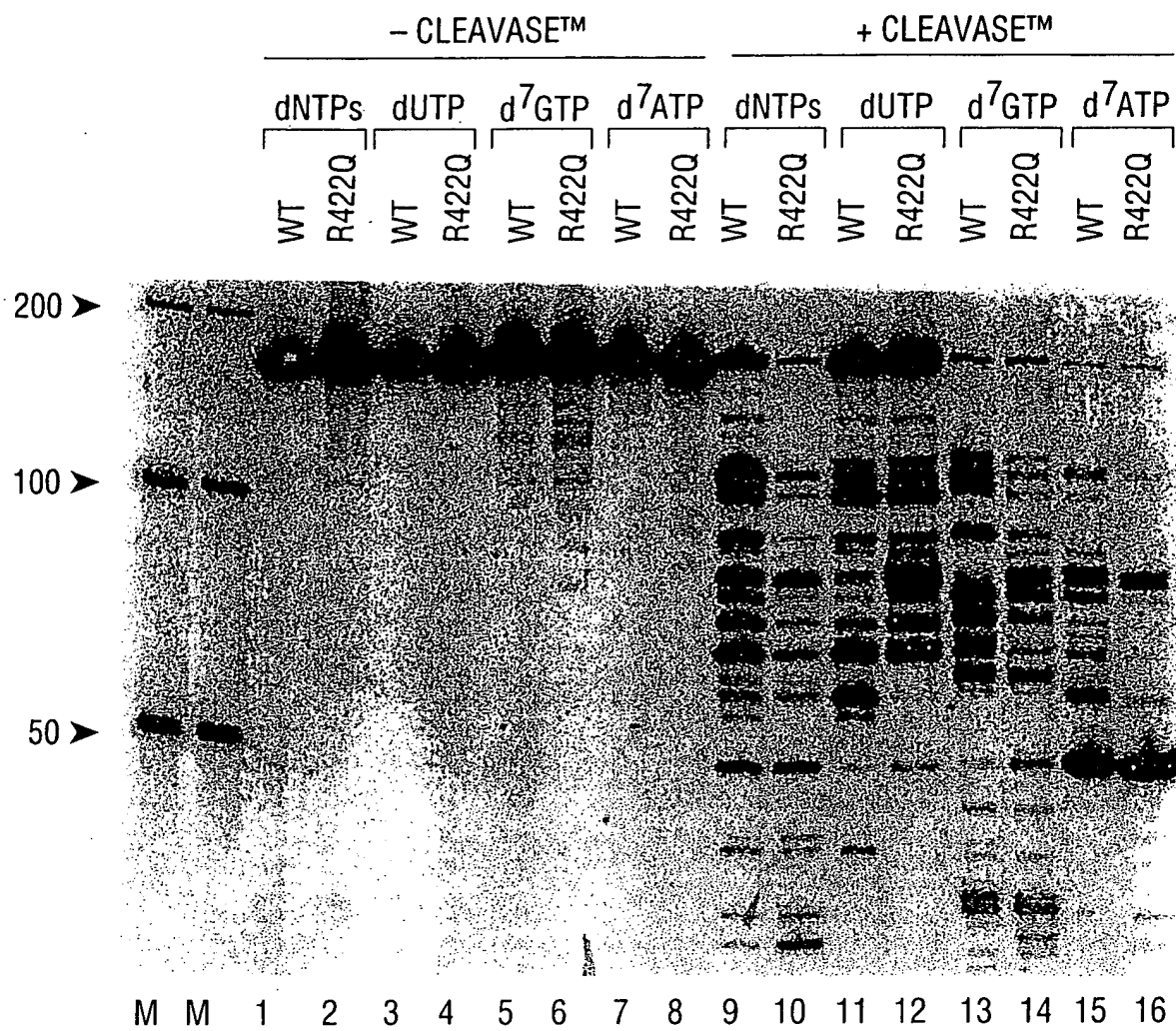


FIG. 94

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